SEQUENCE LISTING

<110> Fischer, Robert L.
      Choi, Yeonhee
      Hannon, Mike
      Okamuro, Jack Kishiro
      Tatarinova, Tatiana Valerievna
      The Regents of the University of California

<120> Nucleic Acids That Control Plant Development

<130> 023070-099910US

<140> US 09/840,743
<141> 2001-04-23

<150> US 09/553,690
<151> 2000-04-21

<160> 119

<170> PatentIn Ver. 2.1

<210> 1
<211> 12785
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DEMETER (DMT) genomic sequence

<400> 1
aagcttaaag ctaccaacat cgaatttagt aaaagaccca tgatttgaaa ttggaattgt 60
cggcaaaatc gagaagatat agagccgaca cgggaacagt gaaaaccaca aagcgcgtaa 120
gaatgaaaca gtgggagaag gaagagagaa tcttaccgat cattcgaggg aaaagatggg 180
aatcagagaa aaatctggaa aaaaagaaat taagagaaag agagagaaga aagtgaggag 240
gaagatgcag tgaagactgc tatagccaca tcccacatgg tgtgatgaga gagagagaga 300
gagaggttaa agcagcaaat tgtggagaga taaagagaga gagagactga gcgagtcaag 360
ttcgtcgtcg tgtttaaaag aaagaatcct atatttgcct ttttctttac tactttatt 420
tcagactatt tgcttatttt gcctcaaact tttttgattg tcacttttcg atcctaaagt 480
gtttgacaat ttacctgcct ttttctccaa gaaaaatcag aacagaccac agcaaattta 540
tgtattttct attaaaaaag aaagaaagaa ttcatattac ttatagaatt aaaagctaag 600
cagttgaaaa cgtgaaagca gaatttctaa aaaaaatagt aaactgctac aaacttattt 660
atgtgtatat aacatatcta taaagaaact caaatatatg ataaatcatt ttaacaaaat 720
ttctatgaaa ttataataaa aaaagtcact tttgacactt aaaaggttga caataaccgt 780
ctctccaaaa aaaaatcaaa acatttataa tttctaaaac tatggtgtaa tttttgctgaa 840
atcaaaaaga aagaaggat ttctatatca taagtttcat tattgtatca aactttcaaa 900
tttcatgtaa tttgaaagga aaaaaattaa gatataatgt tgttttttgtt tcttatgtta 960
catttttcatg gaatatatat tcataacaaa aaatgtattt taatatgatg agagattacc 1020
atccaaaagg tcgaacttat ataaaacaag ttaataacta aacaatacat gtgatcacaa 1080
tcaatgacag ttttgatctt aaaatagaaa tgattgagca aacctcaaaa atgtcttctt 1140
aggatcacaa aatctttcct ttagcttatt aaagccggga gttcaactct ctctcccttg 1200
tagacttttt gttttcaaat cttttttcttt caaaaaatca ataattagtt aatgggcata 1260
atatttggtt ttaattaagt ccatagattt tttaggacca tctctaatca cgacaaatat 1320
cctaaattgt aacacattta aaacttaaaa gtattgcatt cacaatcctt aaaatatata 1380
tatatatata tatatatata tatatatata tattgaaag ttatatagaa acgataactc 1440
cttactcaac aattagccca aaaaaacatc cataatgcat ttaaactagg aattttaaca 1500
aactcaaata ggttggtagt taaaaaaaaa caaatagtag atgtacatac gtaccttaa 1560
aaatatatac tcatatcgaa agttttaaat tttgcgaaat taaatacatt tatctatcaa 1620
ttaaaataca tttaataatg cataattctg taatatctat ctttaatttc catatagaac 1680
caaaacaaaa taaacatatc aaatagtttt aacttaacaa aaacgttagg gaaaagttga 1740

1

```
cctaactagc ttgattgacg ttgaacttgt caatgcgaaa gcgatatttc caatatatac 1800
tacatgtagt attatttata tggaagtttc taaaaaggtg ttgagtggat tgttacttgt 1860
tggaggatgc tatttttttcc ttcttgccat aatattttac gagtatggga taactacata 1920
ctcatgatta tgaaacgctc actttatttg aaaaacctcc taatacacca aatatgtcac 1980
tagattccaa aacgtagacc aattgtatct aatctcaaat tctcaatcaa agtattaatt 2040
taccgatggt aagaaaagtt aaccgatata attatcaaaa gaaagaataa gtcaacagat 2100
tcttaatctc tttattttgg tatatgaaca tttgtacaaa aatctcaaaa gatatgtaac 2160
tgtttaaaat ataaattcac tgagattaat tcttcagact cgtgttagct ataataatgt 2220
caagagttct tcttgtttca aggaaaaacc ttaaagatat gtatattttc tgtaattatg 2280
atgatataat ttgctattca ttgtcacaaa cattactttta aaaaatcgta ttttcattac 2340
tacaatgttg actaagaaca aaaatacatt gattattgat atatcgtcaa ctgaattttc 2400
ttccgaggga tataattctc aaacatagca agaatctcat aataatgttt cgtgactacc 2460
tttagacgaa attttttttaa gattcgtaac gtgacttatg gtctcttgct gtggggtca 2520
atgcgaataa atctaaatgt atgggagtca aataaaatac caagaaaaat aaaggagcag 2580
cacccaataa actatatggg accagaaatc ctttcattgg tttaaaatag gattatcccg 2640
aaagatgaag gactaaattg aaactgattg ggggtaggaa gagatccgtc acaatcatta 2700
atggcttcca cgcggaaact tgtcgtttat acaatttcat taactttcgg gtcgggttta 2760
tattccaaat gggtcaaata atattagttt aatacactaa cggagtaatt aattggtgac 2820
tacaatttta tcagtttggt gcaattagaa acgaacatag tcgtaaaata cgagttcggt 2880
gttataccttt tatttacgtt aaaaaaatac gagaattttg tgtcaaattt caaattaatt 2940
tcatgaatat atggaaatta ttagatactc tagcgaaaat agtgattatg agcgttttac 3000
aaaaatacga ttttagcatt gaacttcctt tatgtaattc ggtcaaatgt tggcatgaag 3060
aagcaagttt gcaacattaa atttcattta aaaatcgtgt tgacatactt taaaatctaa 3120
atataggaag aagaccaaaa cattaaattt agtaagattc taatgaacat ttataagtta 3180
taacttataa ccaacaaaag ttgggtttag cgttgttgct ttatctgaaa acttgcaaac 3240
taaaccattt taataggact aatgacaatt aacaacaaaa tacacttaag caacaacgtc 3300
ctcgtgaata taatttgggc ctcaggccca tattgctaac gccaactgat atttcacttt 3360
attccttctt catctcacca cactctctct ctatctctat ctctaacggc atagctgact 3420
cagtgttctc cggcattgac tcgcctgaga atcagaaagc ttagatcggt gagcttttag 3480
ctccattttc tgtttatttta catattattt ccttttttttc tctctccctt ttttatctgg 3540
aatttgttct gctaaatttt ccagctgtta cattttccga tcacgagaag aatcactggg 3600
ttttttatgtt aatcaataca tgttcctgtt ttctgatcat aaatctcagc tattaacacc 3660
tgatttttgat tctgcgtaat aaaaacctct gatttgcttt tatcttcact ttccccataa 3720
acattgctta ctttattcgc tcttctttta ccgtttccag ctaaaaaatt cttcgctatt 3780
caatgtgttt ctcgtttttgt tgatgagaaa aatatctgac aaaaaatcat ttattgcatt 3840
ttatggtgca gattcttagt taatgtcgcc ttctctaacc aagtcagatt aaaaaggagt 3900
gttcgtccat gttgctttgt tttggtgttt ggagagagtt ttcggagagt taggtgagtg 3960
ttatttgggg tgaggtagtg ataaggtttg aaggggagt gattcatcaa gtgtgttatg 4020
aattcgaggg ctgatccggg ggatagatat tttcgagttc ctttggagaa tcaaactcaa 4080
caagagttca tgggttcttg gattccattt acacccaaaa aacctagatc aagtctgatg 4140
gtagatgaga gagtgataaa ccaggatcta aatgggtttc caggtggtga atttgtagac 4200
aggggattct gcaacactgg tgtggatcat aatggggttt ttgatcatgg tgctcatcag 4260
ggcgttacca acttaagtat gatgatcaat agcttagcgg gatcacatgc acaagcttgg 4320
agtaatagtg agagagatct tttgggcagg agtgaggtga cttctccttt agcaccagtt 4380
atcagaaaca ccaccggtaa tgtagagccg gtcaatggaa attttacttc agatgtgggt 4440
atggtaaatg gtcctttcac ccagagtggc acttctcaag ctggctataa tgagtttgaa 4500
ttggatgact tgttgaatcc tgatcagatg cccttctcct tcacaagctt gctgagtggt 4560
ggggatagct tattcaaggt tcgtcaatgt gagtgatcaa atctattttc agtttttttt 4620
tttccctttc ttccgttctt gcagtactta gagtagaaca tgaattagaa tatcttaaga 4680
aagtcatggt tttgaacaga tggacctcca gcgtgtaaca agcctcttta caatttgaat 4740
tcaccaatta gaagagaagc agttgggtca gtctgtgaaa gttcgtttca atatgtaccg 4800
tcaacgccca gtctgttcag aacaggtgaa aagactggat tccttgaaca gatagttaca 4860
actactggac atgaaatccc agagccgaaa tctgacaaaa gtatgcagag cattatggac 4920
tcgtctgctg ttaatgcgac ggaagctact gaacaaaatg atggcagcag acaagatgtt 4980
ctggagttcg accttaacaa aactcctcag cagaaaccct ccaaaaggaa aaggaagttc 5040
atgcccaagg tggtcgtgga aggcaaacct aaaagaaagc cacgcaaacc tgcagaactt 5100
cccaaagtgg tcgtggaagg caaacctaaa aggaagccac gcaaagctgc aactcaggaa 5160
aaagtgaaat ctaaagaaac cgggagtgcc aaaaagaaaa atttgaaaga atcagcaact 5220
aaaaagccag ccaatgttgg agatatgagc aacaaaagcc ctgaagtcac actcaaaagt 5280
tgcagaaaag ctttgaattt tgacttggag aatcctggag atgcgaggca aggtgactct 5340
gagtctgaaa ttgtccagaa cagtagtggc gcaaactcgt ttctgagat cagagatgcc 5400
```

2

```
attggtggaa ctaatggtag tttcctggat tcagtgtcac aaatagacaa gaccaatgga 5460
ttgggggcta tgaaccagcc acttgaagtg tcaatgggaa accagccaga taaactatct 5520
acaggagcga aactggccag agaccaacaa cctgatttat tgactagaaa ccagcaatgc 5580
cagttcccag tggcaaccca gaacacccag ttcccaatgg aaaaccaaca agcttggctt 5640
cagatgaaaa accaacttat tggctttcca tttggtaacc agcaacctcg catgaccata 5700
agaaaccagc agccttgctt ggccatgggt aatcaacaac ctatgtatct gataggaact 5760
ccacggcctg cattagtaag tggaaaccag caactaggag gtccccaagg aaacaagcgg 5820
cctatatttt tgaatcacca gacttgttta cctgctggaa atcagctata tggatcacct 5880
acagacatgc atcaacttgt tatgtcaacc ggagggcaac aacatggact actgataaaa 5940
aaccagcaac ctggatcatt aataagaggc cagcagcctt gcgtaccttt gattgaccag 6000
caacctgcaa ctccaaaagg ttttactcac ttgaatcaga tggtagctac cagcatgtca 6060
tcgcctgggc ttcgacctca ttctcagtca caagttccta caacatatct acatgtggaa 6120
tctgtttcca ggattttgaa tgggactaca ggtacatgcc agagaagcag ggctcctgca 6180
tacgattctt tacagcaaga tatccatcaa ggaaataagt acatactttc tcatgagata 6240
tccaatggta atgggtgcaa gaaagcgtta cctcaaaact cttctctgcc aactccaatt 6300
atggctaaac ttgaggaagc caggggctcg aagagacagt atcatcgtgc aatgggacag 6360
acggaaaagc atgatctaaa cttagctcaa cagattgctc aatcacaaga tgtggagaga 6420
cataacagca gcacgtgtgt ggaatattta gatgctgcaa agaaaacgaa aatccagaaa 6480
gtagtccaag aaaatttgca tggcatgcca cctgaggtta tagaaatcga ggatgatcca 6540
actgatgggg caagaaaagg taaaaatact gccagcatca gtaaaggtgc atctaaagga 6600
aactcgtctc cagttaaaaa gacagcagaa aaggagaaat gtattgtccc aaaaacgcct 6660
gcaaaaaagg gtcgagcagg tagaaaaaaa tcagtacctc cgcctgctca tgcctcagag 6720
atccagcttt ggcaacctac tcctccaaag acacctttat caagaagcaa gcctaaagga 6780
aaagggagaa agtccataca agattcagga aaagcaagag gtaactaatg tattctacaa 6840
tctctgtgat ataattttga gattttagta actgatgtgt ccaaaccagc tccttatcac 6900
tgttggtgcg ttgtataggt ccatcaggag aacttctgtg tcaggattct attgcggaaa 6960
taatttacag gatgcaaaat ctgtatctag gagacaaaga aagagaacaa gagcaaaatg 7020
caatggtctt gtacaaagga gatggtgcac ttgttcccta tgagagcaag aagcgaaaac 7080
caagacccaa agttgacatt gacgatgaaa caactcgcat atggaactta ctgatgggga 7140
aaggagatga aaaagaaggg gatgaagaga aggataaaaa gaaagagaag tggtgggaag 7200
aagaaagaag agtcttccga ggaagggctg attccttcat cgctcgcatg cacctggtac 7260
aaggtgaaga tccacttctc ttctcaactc cattttttatt cacacaaatt agtagaatac 7320
tcaaaaatga tgttttgttt gcaaaatttt aaaattcact agttaaccat gtcaaataat 7380
attcataatg catcttgtga agaacaggtg tgcatttatg gtgacagctg aatggtttat 7440
gtgcctatta tttcttttac tgctatagat gaccaattga acttaaacgt ttacaggaga 7500
tagacgtttt tcgccatgga agggatcggt ggttgattcg tcattggag ttttccttac 7560
acagaatgtc tcggatcacc tttcaaggta tatgagttgc cttaataaat tgagttccaa 7620
aacatagaaa ttaacccatg gtggttttac aatgcagctc tgcgttcatg tctctagctg 7680
ctcgattccc tccaaaatta agcagcagcc gagaagatga aaggaatgtt agaagcgtag 7740
ttgttgaaga tccagaagga tgcattctga acttaaatga aattccttcg tggcaggaaa 7800
aggttcaaca tccatctgac atggaagttt ctggggttga tagtggatca aaagagcagc 7860
taagggactg ttcaaactct ggaattgaaa gatttaattt cttagagaag agtattcaaa 7920
atttagaaga ggaagtatta tcatcacaag attctttttga tccggcgata tttcagtcgt 7980
gtgggagagt tggatcctgt tcatgttcca aatcagacgc agagtttcct acaaccaggt 8040
gtgaaacaaa aactgtcagt ggaacatcac aatcagtgca aactgggagc ccaaacttgt 8100
ctgatgaaat ttgtcttcaa gggaatgaga gaccgcatct atatgaagga tctggtgatg 8160
ttcagaaaca agaaactaca aatgtcgctc agaagaaacc tgatcttgaa aaaacaatga 8220
attggaaaga ctctgtctgt tttggtcagc caagaaatga tactaattgg caaacaactc 8280
cttccagcag ctatgagcag tgtgcgactc gacagccaca tgtactagac atagaggatt 8340
ttggaatgca gggtgaaggc cttggttatt cttggatgtc catctcacca agagttgaca 8400
gagtaaagaa caaaaatgta ccacgcaggt ttttcagaca aggtggaagt gttccaagag 8460
aattcacagg tcagatcata ccatcaacgc ctcatgaatt accaggaatg ggattgtccg 8520
gttcctcaag cgccgtccaa gaacaccagg acgatataccca acataatcaa caagatgaga 8580
tgaataaagc atcccattta caaaaaacat ttttggatct gctcaactcc tctgaagaat 8640
gccttacaag acagtccagt accaaacaga acatcacgga tggctgtcta ccgagagata 8700
gaactgctga agacgtggtt gatccgctca gtaacaattc aagcttacag aacatattgg 8760
tcgaatcaaa ttccagcaat aaagagcaga cggcagttga atacaaggag acaaatgcca 8820
ctattttacg agagatgaaa gggacgcttg ctgatgggaa aaagcctaca agccagtggg 8880
atagtctcag aaaagatgtg gaggggaatg aagggagaca ggaacgaaac aaaaacaata 8940
tggattccat agactatgaa gcaataagac gtgctagtat cagcgagatt tctgaggcta 9000
tcaaggaaag agggatgaat aacatgttgg ccgtacgaat taaggtaaat ctactaattt 9060
```

3

```
cagttgagac cctcatcaaa tctgtcagaa ggcttgaaca tcagtaaatt atgtaaccat 9120
atttacaaca ttgcaggatt tcctagaacg gatagttaaa gatcatggtg gtatcgacct 9180
tgaatggttg agagaatctc ctcctgataa agccaagtgg gtaaatcaca tttttagtga 9240
ctgcaacact agcacgatcg atttactcaa caattacgtc aaactgagta ttaacaagtt 9300
gctcatgaac atttcacagg gactatctct tgagcataag aggtctgggt ttgaaaagtg 9360
ttgaatgcgt gcgactctta acactccaca atcttgcttt ccctgtgagt cagactattc 9420
cattatctac taaaaactta gaataactcc ggctaactaa gctggaactt gtattgatga 9480
tatgaaggtt gacacgaatg ttggaaggat agcagttagg atgggatggg tgcctctaca 9540
acccctacct gaatcacttc agttacacct cctggagctg taagtttctt tttgtttgtc 9600
atctaaacaa cgaaattttt atgcaagtca taaccatgct gtgttttcac agatacccag 9660
tgctcgagtc catccaaaaa tttctttggc caagactttg caaactcgat caacgaacac 9720
tgtatgctca taaactctaa caaatcatct gtctgaaaaa ccaatatttc tttggtagaa 9780
ttctattgtc attactcatt actaacagcg aaattaatta acgttctttt tcttactcag 9840
gtatgaatta cactaccaac tgattacgtt tggaaaggta ttattgctct aagctttgaa 9900
tttatcatat ggtaatttca agcattgtag gcacctgatc aattatgtgt ctaaatcatg 9960
tgaattcatg tcaggtattt tgcacaaaga gtagaccaaa ttgtaatgca tgtccaatga 10020
gaggagagtg cagacacttt gccagtgctt atgctaggta agcaagcttt catgtactta 10080
tatgcaataa ttaaagataa aatttaggat tatgggtaag ttacaaaaaa ttaggctcag 10140
tttcatggta gctagctgga aatagtatta caagaacaac ataaagatca aagacagaat 10200
catggatcca tatgcactat cattttagct cttgtaatcc atacatgaac actatatgcc 10260
aaagtaggga tttcaaatat gagattcgat gactgatgcc attgtaacag tgcaagactt 10320
gctttaccgg caccagagga gaggagctta acaagtgcaa ctattccggt ccctcccgag 10380
tcctatcctc ctgtagccat cccgatgata gaactacctc ttccgttgga gaaatcccta 10440
gcaagtggag caccatcgaa tagagaaaac tgtgaaccaa taattgaaga gccggcctcg 10500
cccgggcaag agtgcactga aataaccgag agtgatattg aagatgctta ctacaatgag 10560
gaccctgacg agatcccaac aataaaactc aacattgaac agtttggaat gactctacgg 10620
gaacacatgg aaagaaacat ggagctccaa gaaggtgaca tgtccaaggc tttggttgct 10680
ttgcatccaa caactacttc tattccaact cccaaactaa agaacattag ccgtctcagg 10740
acagagcacc aagtgtaagc taatatctcc tcctatattt tatcttccat ataaattttg 10800
gggaaaaaat cgctctccat ctggttttag aacatgcggg tcagccaggg ttatggcatt 10860
tttatatatt tcaccgatcg gcccgagctg gctctggttg actcgtatgc caccctgcat 10920
tgaacaaacc agtaggagac aagcaagcaa aacgttttaa gataaggtct atggtaaaat 10980
gacaaggtaa ctgataaatg tgtcgtctat ttgcaggtac gagctcccag attcacatcg 11040
tctccttgat ggtgtaagtc aatttttaac tctctctata ctcgagttgt ttcacttgag 11100
caacactgtt taaaagtcct catttgataa aataacagat ggataaaaga gaaccagatg 11160
atccaagtcc ttatctctta gctatatgga caccaggtga gaataaaact gcaatgtttc 11220
attcatgtgt ctacagtatc aaagaaagta cagctagagc taaaaagcat ttgaaataga 11280
gtcggttaaa tatgaaagtt tgaatctgta aatgaaagcc ggaacgtagc attggtggat 11340
gttatatgta aattagtttt tgagattggt ctaatgtagt tgtttgactg ccaggtgaaa 11400
cagcgaattc ggcacaaccg cctgaacaga agtgtggagg gaaagcgtct ggcaaaatgt 11460
gctttgacga gacttgttct gagtgtaaca gtctgaggga agcaaactca cagacagttc 11520
gaggaactct tctggtgaga ttatcttgat ctttttgtgtt gctcatgaaa aggagaagtg 11580
agaatacaag tttgctaata tcattttttc gtcattcaca gataccttgt cggactgcca 11640
tgagaggaag ttttccgctc aacgggacat atttccaagt caacgaggtt agatgaaata 11700
aaactcaaac agacagacga aacattattt ctgtttagtg ttggttcttt atcctccttg 11760
ccatttttta tcttgcagtt atttgcagac cacgagtcca gtctcaaacc catcgatgtt 11820
cctagagatt ggatatggga tctcccaaga aggactgttt acttcggaac atcagtaaca 11880
tcaatattca gaggtaaaaa cattcgtaat agagttagtt aatcaaatgt ccaaaacaca 11940
agaaagcttc accgtccaat acacaagaaa gcttcacctt ctctttgcca aaaaagatct 12000
tagaatgttt tgctgaattt gtgcaggtct ttcaacggag cagatacagt tctgcttttg 12060
gaaaggtaaa cgttaacttt cgacccagag aaatccggaa aatctattgc tttgttctga 12120
tcaatacgtt aaacatatac acacacactt tacacttagg accaatactg ttctgatctg 12180
tgatagaaac tggtaaacat ctaacaatta tgattgcagg attcgtatgt gtccgtggat 12240
tcgaacagaa gacaagagca ccgcgtccat taatggcaag gttgcatttt cctgcgagca 12300
aattgaagaa caacaaaacc taaagatgac tggaagaaag caaacgcatt gcttctctgc 12360
tctcctctat ttaaagccag gaaaagtccc atttagacat aataacagga atccaaatag 12420
gctattttct ctttctttct tatttcattc atagagcaga agcgacacaa aaaagttttt 12480
tgggttattt attttctctc taacaaattt gtagcgtttt gggtcttttt ctggctgtca 12540
ctagcgtggc aaatccaatg tccgcgcaca cttaggcgca ttgtcaataa attctccggc 12600
caccggagtg ttacgatctt ttccaacggc ggctaatgcg atatttccgg taacacatat 12660
tccttattct atgttggttt tgtgtacggc gtgggcctta ctagacaatg atcatcaata 12720
```

4

aaactaacac aaagttgaat gctacaaagt agaaagtgaa gaaaaaataa tatagacatt 12780
gccga   12785

<210> 2
<211> 1729
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DEMETER (DMT)

<400> 2

```
Met Gln Ser Ile Met Asp Ser Ser Ala Val Asn Ala Thr Glu Ala Thr
  1               5                  10                  15

Glu Gln Asn Asp Gly Ser Arg Gln Asp Val Leu Glu Phe Asp Leu Asn
             20                  25                  30

Lys Thr Pro Gln Gln Lys Pro Ser Lys Arg Lys Arg Lys Phe Met Pro
         35                  40                  45

Lys Val Val Val Glu Gly Lys Pro Lys Arg Lys Pro Arg Lys Pro Ala
     50                  55                  60

Glu Leu Pro Lys Val Val Val Glu Gly Lys Pro Lys Arg Lys Pro Arg
 65                  70                  75                  80

Lys Ala Ala Thr Gln Glu Lys Val Lys Ser Lys Glu Thr Gly Ser Ala
             85                  90                  95

Lys Lys Lys Asn Leu Lys Glu Ser Ala Thr Lys Lys Pro Ala Asn Val
            100                 105                 110

Gly Asp Met Ser Asn Lys Ser Pro Glu Val Thr Leu Lys Ser Cys Arg
            115                 120                 125

Lys Ala Leu Asn Phe Asp Leu Glu Asn Pro Gly Asp Ala Arg Gln Gly
        130                 135                 140

Asp Ser Glu Ser Glu Ile Val Gln Asn Ser Ser Gly Ala Asn Ser Phe
145                 150                 155                 160

Ser Glu Ile Arg Asp Ala Ile Gly Gly Thr Asn Gly Ser Phe Leu Asp
                165                 170                 175

Ser Val Ser Gln Ile Asp Lys Thr Asn Gly Leu Gly Ala Met Asn Gln
            180                 185                 190

Pro Leu Glu Val Ser Met Gly Asn Gln Pro Asp Lys Leu Ser Thr Gly
        195                 200                 205

Ala Lys Leu Ala Arg Asp Gln Gln Pro Asp Leu Leu Thr Arg Asn Gln
    210                 215                 220

Gln Cys Gln Phe Pro Val Ala Thr Gln Asn Thr Gln Phe Pro Met Glu
225                 230                 235                 240

Asn Gln Gln Ala Trp Leu Gln Met Lys Asn Gln Leu Ile Gly Phe Pro
                245                 250                 255
```

5

```
Phe Gly Asn Gln Gln Pro Arg Met Thr Ile Arg Asn Gln Gln Pro Cys
        260             265             270

Leu Ala Met Gly Asn Gln Gln Pro Met Tyr Leu Ile Gly Thr Pro Arg
        275             280             285

Pro Ala Leu Val Ser Gly Asn Gln Gln Leu Gly Gly Pro Gln Gly Asn
    290             295             300

Lys Arg Pro Ile Phe Leu Asn His Gln Thr Cys Leu Pro Ala Gly Asn
305             310             315             320

Gln Leu Tyr Gly Ser Pro Thr Asp Met His Gln Leu Val Met Ser Thr
            325             330             335

Gly Gly Gln Gln His Gly Leu Leu Ile Lys Asn Gln Gln Pro Gly Ser
        340             345             350

Leu Ile Arg Gly Gln Gln Pro Cys Val Pro Leu Ile Asp Gln Gln Pro
        355             360             365

Ala Thr Pro Lys Gly Phe Thr His Leu Asn Gln Met Val Ala Thr Ser
    370             375             380

Met Ser Ser Pro Gly Leu Arg Pro His Ser Gln Ser Gln Val Pro Thr
385             390             395             400

Thr Tyr Leu His Val Glu Ser Val Ser Arg Ile Leu Asn Gly Thr Thr
            405             410             415

Gly Thr Cys Gln Arg Ser Arg Ala Pro Ala Tyr Asp Ser Leu Gln Gln
        420             425             430

Asp Ile His Gln Gly Asn Lys Tyr Ile Leu Ser His Glu Ile Ser Asn
        435             440             445

Gly Asn Gly Cys Lys Lys Ala Leu Pro Gln Asn Ser Ser Leu Pro Thr
450             455             460

Pro Ile Met Ala Lys Leu Glu Glu Ala Arg Gly Ser Lys Arg Gln Tyr
465             470             475             480

His Arg Ala Met Gly Gln Thr Glu Lys His Asp Leu Asn Leu Ala Gln
            485             490             495

Gln Ile Ala Gln Ser Gln Asp Val Glu Arg His Asn Ser Ser Thr Cys
        500             505             510

Val Glu Tyr Leu Asp Ala Ala Lys Lys Thr Lys Ile Gln Lys Val Val
        515             520             525

Gln Glu Asn Leu His Gly Met Pro Pro Glu Val Ile Glu Ile Glu Asp
    530             535             540

Asp Pro Thr Asp Gly Ala Arg Lys Gly Lys Asn Thr Ala Ser Ile Ser
545             550             555             560

Lys Gly Ala Ser Lys Gly Asn Ser Ser Pro Val Lys Lys Thr Ala Glu
            565             570             575
```

6

```
Lys Glu Lys Cys Ile Val Pro Lys Thr Pro Ala Lys Lys Gly Arg Ala
            580             585             590

Gly Arg Lys Lys Ser Val Pro Pro Pro Ala His Ala Ser Glu Ile Gln
        595             600             605

Leu Trp Gln Pro Thr Pro Pro Lys Thr Pro Leu Ser Arg Ser Lys Pro
    610             615             620

Lys Gly Lys Gly Arg Lys Ser Ile Gln Asp Ser Gly Lys Ala Arg Gly
625             630             635                 640

Pro Ser Gly Glu Leu Leu Cys Gln Asp Ser Ile Ala Glu Ile Ile Tyr
            645             650             655

Arg Met Gln Asn Leu Tyr Leu Gly Asp Lys Glu Arg Glu Gln Glu Gln
        660             665             670

Asn Ala Met Val Leu Tyr Lys Gly Asp Gly Ala Leu Val Pro Tyr Glu
        675             680             685

Ser Lys Lys Arg Lys Pro Arg Pro Lys Val Asp Ile Asp Asp Glu Thr
    690             695             700

Thr Arg Ile Trp Asn Leu Leu Met Gly Lys Gly Asp Glu Lys Glu Gly
705             710             715             720

Asp Glu Glu Lys Asp Lys Lys Lys Glu Lys Trp Trp Glu Glu Glu Arg
            725             730             735

Arg Val Phe Arg Gly Arg Ala Asp Ser Phe Ile Ala Arg Met His Leu
        740             745             750

Val Gln Gly Asp Arg Arg Phe Ser Pro Trp Lys Gly Ser Val Val Asp
        755             760             765

Ser Val Ile Gly Val Phe Leu Thr Gln Asn Val Ser Asp His Leu Ser
    770             775             780

Ser Ser Ala Phe Met Ser Leu Ala Ala Arg Phe Pro Pro Lys Leu Ser
785             790             795             800

Ser Ser Arg Glu Asp Glu Arg Asn Val Arg Ser Val Val Val Glu Asp
            805             810             815

Pro Glu Gly Cys Ile Leu Asn Leu Asn Glu Ile Pro Ser Trp Gln Glu
            820             825             830

Lys Val Gln His Pro Ser Asp Met Glu Val Ser Gly Val Asp Ser Gly
        835             840             845

Ser Lys Glu Gln Leu Arg Asp Cys Ser Asn Ser Gly Ile Glu Arg Phe
    850             855             860

Asn Phe Leu Glu Lys Ser Ile Gln Asn Leu Glu Glu Glu Val Leu Ser
865             870             875             880

Ser Gln Asp Ser Phe Asp Pro Ala Ile Phe Gln Ser Cys Gly Arg Val
            885             890             895
```

7

```
Gly Ser Cys Ser Cys Ser Lys Ser Asp Ala Glu Phe Pro Thr Thr Arg
        900             905             910

Cys Glu Thr Lys Thr Val Ser Gly Thr Ser Gln Ser Val Gln Thr Gly
        915             920             925

Ser Pro Asn Leu Ser Asp Glu Ile Cys Leu Gln Gly Asn Glu Arg Pro
    930             935             940

His Leu Tyr Glu Gly Ser Gly Asp Val Gln Lys Gln Glu Thr Thr Asn
945             950             955             960

Val Ala Gln Lys Lys Pro Asp Leu Glu Lys Thr Met Asn Trp Lys Asp
            965             970             975

Ser Val Cys Phe Gly Gln Pro Arg Asn Asp Thr Asn Trp Gln Thr Thr
            980             985             990

Pro Ser Ser Ser Tyr Glu Gln Cys Ala Thr Arg Gln Pro His Val Leu
        995             1000            1005

Asp Ile Glu Asp Phe Gly Met Gln Gly Glu Gly Leu Gly Tyr Ser Trp
    1010            1015            1020

Met Ser Ile Ser Pro Arg Val Asp Arg Val Lys Asn Lys Asn Val Pro
1025            1030            1035            1040

Arg Arg Phe Phe Arg Gln Gly Gly Ser Val Pro Arg Glu Phe Thr Gly
            1045            1050            1055

Gln Ile Ile Pro Ser Thr Pro His Glu Leu Pro Gly Met Gly Leu Ser
        1060            1065            1070

Gly Ser Ser Ser Ala Val Gln Glu His Gln Asp Asp Thr Gln His Asn
        1075            1080            1085

Gln Gln Asp Glu Met Asn Lys Ala Ser His Leu Gln Lys Thr Phe Leu
    1090            1095            1100

Asp Leu Leu Asn Ser Ser Glu Glu Cys Leu Thr Arg Gln Ser Ser Thr
1105            1110            1115            1120

Lys Gln Asn Ile Thr Asp Gly Cys Leu Pro Arg Asp Arg Thr Ala Glu
            1125            1130            1135

Asp Val Val Asp Pro Leu Ser Asn Asn Ser Ser Leu Gln Asn Ile Leu
            1140            1145            1150

Val Glu Ser Asn Ser Ser Asn Lys Glu Gln Thr Ala Val Glu Tyr Lys
        1155            1160            1165

Glu Thr Asn Ala Thr Ile Leu Arg Glu Met Lys Gly Thr Leu Ala Asp
    1170            1175            1180

Gly Lys Lys Pro Thr Ser Gln Trp Asp Ser Leu Arg Lys Asp Val Glu
1185            1190            1195            1200

Gly Asn Glu Gly Arg Gln Glu Arg Asn Lys Asn Asn Met Asp Ser Ile
            1205            1210            1215
```

8

Asp Tyr Glu Ala Ile Arg Arg Ala Ser Ile Ser Glu Ile Ser Glu Ala
        1220   1225   1230

Ile Lys Glu Arg Gly Met Asn Asn Met Leu Ala Val Arg Ile Lys Asp
        1235   1240   1245

Phe Leu Glu Arg Ile Val Lys Asp His Gly Gly Ile Asp Leu Glu Trp
    1250   1255   1260

Leu Arg Glu Ser Pro Pro Asp Lys Ala Lys Asp Tyr Leu Leu Ser Ile
1265   1270   1275   1280

Arg Gly Leu Gly Leu Lys Ser Val Glu Cys Val Arg Leu Leu Thr Leu
            1285   1290   1295

His Asn Leu Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile Ala Val
        1300   1305   1310

Arg Met Gly Trp Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu
        1315   1320   1325

His Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Ile Gln Lys Phe Leu
        1330   1335   1340

Trp Pro Arg Leu Cys Lys Leu Asp Gln Arg Thr Leu Tyr Glu Leu His
1345   1350   1355   1360

Tyr Gln Leu Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Arg Pro
            1365   1370   1375

Asn Cys Asn Ala Cys Pro Met Arg Gly Glu Cys Arg His Phe Ala Ser
            1380   1385   1390

Ala Tyr Ala Ser Ala Arg Leu Ala Leu Pro Ala Pro Glu Glu Arg Ser
        1395   1400   1405

Leu Thr Ser Ala Thr Ile Pro Val Pro Pro Glu Ser Phe Pro Pro Val
    1410   1415   1420

Ala Ile Pro Met Ile Glu Leu Pro Leu Pro Leu Glu Lys Ser Leu Ala
1425   1430   1435   1440

Ser Gly Ala Pro Ser Asn Arg Glu Asn Cys Glu Pro Ile Ile Glu Glu
            1445   1450   1455

Pro Ala Ser Pro Gly Gln Glu Cys Thr Glu Ile Thr Glu Ser Asp Ile
        1460   1465   1470

Glu Asp Ala Tyr Tyr Asn Glu Asp Pro Asp Glu Ile Pro Thr Ile Lys
        1475   1480   1485

Leu Asn Ile Glu Gln Phe Gly Met Thr Leu Arg Glu His Met Glu Arg
        1490   1495   1500

Asn Met Glu Leu Gln Glu Gly Asp Met Ser Lys Ala Leu Val Ala Leu
1505   1510   1515   1520

His Pro Thr Thr Thr Ser Ile Pro Thr Pro Lys Leu Lys Asn Ile Ser
            1525   1530   1535

9

```
Arg Leu Arg Thr Glu His Gln Val Tyr Glu Leu Pro Asp Ser His Arg
        1540                1545                1550

Leu Leu Asp Gly Met Asp Lys Arg Glu Pro Asp Asp Pro Ser Pro Tyr
        1555                1560                1565

Leu Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ala Gln Pro
    1570                1575                1580

Pro Glu Gln Lys Cys Gly Gly Lys Ala Ser Gly Lys Met Cys Phe Asp
1585                1590                1595                1600

Glu Thr Cys Ser Glu Cys Asn Ser Leu Arg Glu Ala Asn Ser Gln Thr
            1605                1610                1615

Val Arg Gly Thr Leu Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser
        1620                1625                1630

Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Leu Phe Ala Asp
        1635                1640                1645

His Glu Ser Ser Leu Lys Pro Ile Asp Val Pro Arg Asp Trp Ile Trp
    1650                1655                1660

Asp Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser Val Thr Ser Ile
1665                1670                1675                1680

Phe Arg Gly Leu Ser Thr Glu Gln Ile Gln Phe Cys Phe Trp Lys Gly
            1685                1690                1695

Phe Val Cys Val Arg Gly Phe Glu Gln Lys Thr Arg Ala Pro Arg Pro
        1700                1705                1710

Leu Met Ala Arg Leu His Phe Pro Ala Ser Lys Leu Lys Asn Asn Lys
    1715                1720                1725

Thr


<210> 3
<211> 3424
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT 5' flanking sequence

<400> 3
aagcttaaag ctaccaacat cgaatttagt aaaagaccca tgatttgaaa ttggaattgt 60
cggcaaaatc gagaagatat agagccgaca cgggaacagt gaaaaccaca aagcgcgtaa 120
gaatgaaaca gtgggagaag gaagagagaa tcttaccgat cattcgaggg aaaagatggg 180
aatcagagaa aaatctggaa aaaaagaaat taagagaaag agagagaaga aagtgaggag 240
gaagatgcag tgaagactgc tatagccaca tcccacatgg tgtgatgaga gagagagaga 300
gagaggttaa agcagcaaat tgtggagaga taaagagaga gagagactga gcgagtcaag 360
ttcgtcgtcg tgtttaaaag aaagaatcct atatttgcct ttttctttac tactttattt 420
tcagactatt tgcttatttt gcctcaaact tttttgattg tcacttttcg atcctaaagt 480
gtttgacaat ttacctgcct ttttctccaa gaaaaatcag aacagaccac agcaaattta 540
tgtattttct attaaaaaag aaagaaagaa ttcatattac ttatagaatt aaaagctaag 600
cagttgaaaa cgtgaaagca gaatttctaa aaaaaatagt aaactgctac aaacttattt 660
atgtgtatat aacatatcta taaagaaact caaatatatg ataaatcatt ttaacaaaat 720
```

10

```
ttctatgaaa ttataataaa aaaagtcact tttgacactt aaaaggttga caataaccgt 780
ctctccaaaa aaaaatcaaa acatttataa tttctaaaac tatggtgtaa ttttgctgaa 840
atcaaaaaga aaagaaggat ttctatatca taagtttcat tattgtatca aactttcaaa 900
tttcatgtaa tttgaaagga aaaaaattaa gatataatgt tgttttttgtt tcttatgtta 960
cattttcatg gaatatatat tcataacaaa aaatgtattt taatatgatg agagattacc 1020
atccaaaagg tcgaacttat ataaaacaag ttaataacta aacaatacat gtgatcacaa 1080
tcaatgacag ttttgatctt aaaatagaaa tgattgagca aacctcaaaa atgtcttctt 1140
aggatcacaa aatctttcct ttagcttatt aaagccggga gttcaactct ctctcccttg 1200
tagacttttt gttttcaaat ctttttcttt caaaaaatca ataattagtt aatgggcata 1260
atatttggtt ttaattaagt ccatagattt tttaggacca tctctaatca cgacaaatat 1320
cctaaattgt aacacattta aaacttaaaa gtattgcatt cacaatcctt aaaatatata 1380
tatatatata tatatatata tatatatata tatgaaag ttatatagaa acgataactc 1440
cttactcaac aattagccca aaaaaacatc cataatgcat ttaaactagg aattttaaca 1500
aactcaaata ggttggtagt taaaaaaaaa caaatagtag atgtacatac gtacctttaa 1560
aaatatatac tcatatcgaa agttttaaat tttgcgaaat taaatacatt tatctatcaa 1620
ttaaaataca tttaataatg cataattctg taatatctat ctttaatttc catatagaac 1680
caaaacaaaa taaacatatc aaatagtttt aacttaacaa aaacgttagg gaaaagttga 1740
cctaactagc ttgattgacg ttgaacttgt caatgcgaaa gcgatatttc caatatatac 1800
tacatgtagt attatttata tggaagtttc taaaaaggtg ttgagtggat tgttacttgt 1860
tggaggatgc tatttttttcc ttcttgccat aatatttac gagtatggga taactacata 1920
ctcatgatta tgaaacgctc actttatttg aaaaacctcc taatacacca aatatgtcac 1980
tagattccaa aacgtagacc aattgtatct aatctcaaat tctcaatcaa agtattaatt 2040
taccgatggt aagaaaagtt aaccgatata attatcaaaa gaaagaataa gtcaacagat 2100
tcttaatctc tttattttgg tatatgaaca tttgtacaaa aatctcaaaa gatatgtaac 2160
tgtttaaaat ataaattcac tgagattaat tcttcagact cgtgttagct ataataatgt 2220
caagagttct tcttgtttca aggaaaaacc ttaaagatat gtatattttc tgtaattatg 2280
atgatataat ttgctattca ttgtcacaaa cattacttta aaaaatcgta ttttcattac 2340
tacaatgttg actaagaaca aaaatacatt gattattgat atatcgtcaa ctgaattttc 2400
ttccgaggga tataattctc aaacatagca agaatctcat aataatgttt cgtgactacc 2460
tttagacgaa attttttaa gattcgtaac gtgacttatg gtctcttgct gtggggggtca 2520
atgcgaataa atctaaatgt atgggagtca aataaaatac caagaaaaat aaaggagcag 2580
cacccaataa actatatggg accagaaatc ctttcattgg tttaaaatag gattatcccg 2640
aaagatgaag gactaaattg aaactgattg ggggtaggaa gagatccgtc acaatcatta 2700
atggcttcca cgcggaaact tgtcgtttat acaatttcat taactttcgg gtcgggttta 2760
tattccaaat gggtcaaata atattagttt aatacactaa cggagtaatt aattggtgac 2820
tacaattttta tcagtttggt gcaattagaa acgaacatag tcgtaaaata cgagttcggt 2880
gttatacctt tatttacgtt aaaaaaatac gagaattttg tgtcaaattt caaattaatt 2940
tcatgaatat atggaaatta ttagatactc tagcgaaaat agtgattatg agcgttttac 3000
aaaaatacga ttttagcatt gaacttcctt tatgtaattc ggtcaaatgt tggcatgaag 3060
aagcaagttt gcaacattaa atttcattta aaaatcgtgt tgacatactt aaaatctaa 3120
atataggaag aagaccaaaa cattaaattt agtaagattc taatgaacat ttataagtta 3180
taacttataa ccaacaaaag ttgggtttag cgttgttgct ttatctgaaa acttgcaaac 3240
taaaccattt taataggact aatgacaatt aacaacaaaa tacacttaag caacaacgtc 3300
ctcgtgaata taatttgggc ctcaggccca tattgctaac gccaactgat atttcacttt 3360
attccttctt catctcacca cactctctct ctatctctat ctctaacggc atagctgact 3420
cagt                                                                3424
```

```
agatgactgg aagaaagcaa acgcattgct tctctgctct cctctatttta aagccaggaa 60
aagtcccatt tagacataat aacaggaatc caaataggct attttctctt tctttcttat 120
ttcattcata gagcagaagc gacacaaaaa agttttttgg gttatttatt ttctctctaa 180
caaaaaaaaa aaaaaaaaac tcgag                                       205
```

<210> 5
<211> 6873
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT cDNA

<400> 5
```
gttctccggc attgactcgc ctgagaatca gaaagcttag atcggtgagc ttttagctcc 60
attttctgtt tatttacata ttatttcctt tttttctctc tcccttttt atctggaatt 120
tgttctgcta aattttccag ctgttacatt ttccgatcac gagaagaatc actgggtttt 180
tatgttaatc aatacatgtt cctgttttct gatcataaat ctcagctatt aacacctgat 240
tttgattctg cgtaataaaa acctctgatt tgcttttatc ttcactttcc ccataaacat 300
tgcttacttt attcgctctt cttttaccgt ttccagctaa aaaattcttc gctattcaat 360
gtgtttctcg ttttgttgat gagaaaaata tctgacaaaa aatcatttat tgcattttat 420
ggtgcagatt cttagttaat gtcgccttct ctaaccaagt cagattaaaa aggagtgttc 480
gtccatgttg cttgttttg gtgtttggag agagttttcg gagagttagg tgagtgttat 540
ttggggtgag gtagtgataa ggtttgaagg gggagtgatt catcaagtgt gttatgaatt 600
cgagggctga tccggggggat agatattttc gagttccttt ggagaatcaa actcaacaag 660
agttcatggg ttcttggatt ccatttacac ccaaaaaacc tagatcaagt ctgatggtag 720
atgagagagt gataaaccag gatctaaatg ggtttccagg tggtgaattt gtagacaggg 780
gattctgcaa cactggtgtg gatcataatg gggttttga tcatggtgct catcagggcg 840
ttaccaactt aagtatgatg atcaatagct tagcgggatc acatgcacaa gcttggagta 900
atagtgagag agatcttttg ggcaggagtg aggtgacttc tcctttagca ccagttatca 960
gaaacaccac cggtaatgta gagccggtca atggaaattt tacttcagat gtgggtatgg 1020
taaatggtcc tttcacccag agtggcactt ctcaagctgg ctataatgag tttgaattgg 1080
atgacttgtt gaatcctgat cagatgccct tctccttcac aagcttgctg agtggtgggg 1140
atagcttatt caaggttcgt caatgtgagt gatcaaatct attttcagtt ttttttttc 1200
cctttcttcc gttcttgcag tacttagagt agaacatgaa ttagaatatc ttaagaaagt 1260
catggttttg aacagatgga cctccagcgt gtaacaagcc tctttacaat ttgaattcac 1320
caattagaag agaagcagtt gggtcagtct gtgaaagttc gtttcaatat gtaccgtcaa 1380
cgcccagtct gttcagaaca ggtgaaaaga ctggattcct tgaacagata gttacaacta 1440
ctggacatga aatcccagag ccgaaatctg acaaaagtat gcagagcatt atggactcgt 1500
ctgctgttaa tgcgacggaa gctactgaac aaaatgatgg cagcagacaa gatgttctgg 1560
agttcgacct taacaaaact cctcagcaga aaccctccaa aaggaaaagg aagttcatgc 1620
ccaaggtggt cgtggaaggc aaacctaaaa gaaagccacg caaacctgca gaacttccca 1680
aagtggtcgt ggaaggcaaa cctaaaagga agccacgcaa agctgcaact caggaaaaag 1740
tgaaatctaa agaaaccggg agtgccaaaa agaaaaattt gaaagaatca gcaactaaaa 1800
agccagccaa tgttggagat atgagcaaca aaagccctga agtcacactc aaaagttgca 1860
gaaaagcttt gaattttgac ttggagaatc ctggagatgc gaggcaaggt gactctgagt 1920
ctgaaattgt ccagaacagt agtggcgcaa actcgttttc tgagatcaga gatgccattg 1980
gtggaactaa tggtagtttc ctggattcag tgtcacaaat agacaagacc aatggattgg 2040
gggctatgaa ccagccactt gaagtgtcaa tgggaaacca gccagataaa ctatctacag 2100
gagcgaaact ggccagagac caacaacctg atttattgac tagaaaccag caatgccagt 2160
tcccagtggc aacccagaac acccagttcc caatggaaaa ccaacaagct tggcttcaga 2220
tgaaaaacca acttattggc tttccatttg gtaaccagca acctcgcatg accataagaa 2280
accagcagcc ttgcttggcc atgggtaatc aacaacctat gtatctgata ggaactccac 2340
ggcctgcatt agtaagtgga aaccagcaac taggaggtcc ccaaggaaac aagcggccta 2400
tattttgaa tcaccagact tgtttacctg ctggaaatca gctatatgga tcacctacag 2460
acatgcatca acttgttatg tcaaccggag ggcaacaaca tggactactg ataaaaaacc 2520
agcaacctgg atcattaata agaggccagc agccttgcgt acctttgatt gaccagcaac 2580
ctgcaactcc aaaaggtttt actcacttga tcagatggt agctaccagc atgtcatcgc 2640
ctgggcttcg acctcattct cagtcacaag ttcctacaac atatctacat gtggaatctg 2700
tttccaggat tttgaatggg actacaggta catgccagag aagcagggct cctgcatacg 2760
attctttaca gcaagatatc catcaaggaa ataagtacat actttctcat gagatatcca 2820
atggtaatgg gtgcaagaaa gcgttacctc aaaactcttc tctgccaact ccaattatgg 2880
ctaaacttga ggaagccagg ggctcgaaga gacagtatca tcgtgcaatg ggacagacgg 2940
aaaagcatga tctaaactta gctcaacaga ttgctcaatc acaagatgtg gagagacata 3000
acagcagcac gtgtgtggaa tatttagatg ctgcaaagaa aacgaaaatc cagaaagtag 3060
tccaagaaaa tttgcatggc atgccacctg aggttataga aatcgaggat gatccaactg 3120
```

```
atgggggcaag aaaaggtaaa aatactgcca gcatcagtaa aggtgcatct aaaggaaact 3180
cgtctccagt taaaaagaca gcagaaaagg agaaatgtat tgtcccaaaa acgcctgcaa 3240
aaaagggtcg agcaggtaga aaaaaatcag tacctccgcc tgctcatgcc tcagagatcc 3300
agctttggca acctactcct ccaaagacac ctttatcaag aagcaagcct aaaggaaaag 3360
ggagaaagtc catacaagat tcaggaaaag caagaggtcc atcaggagaa cttctgtgtc 3420
aggattctat tgcggaaata atttacagga tgcaaaatct gtatctagga gacaaagaaa 3480
gagaacaaga gcaaaatgca atggtcttgt acaaaggaga tggtgcactt gttccctatg 3540
agagcaagaa gcgaaaacca agacccaaag ttgacattga cgatgaaaca actcgcatat 3600
ggaacttact gatggggaaa ggagatgaaa aagaagggga tgaagagaag gataaaaaga 3660
aagagaagtg gtgggaagaa gaaagaagag tcttccgagg aagggctgat tccttcatcg 3720
ctcgcatgca cctggtacaa ggagatagac gttttttcgcc atggaaggga tcggtggttg 3780
attcggtcat tggagttttc cttacacaga atgtctcgga tcacctttca agctctgcgt 3840
tcatgtctct agctgctcga ttccctccaa aattaagcag cagccgagaa gatgaaagga 3900
atgttagaag cgtagttgtt gaagatccag aaggatgcat tctgaactta aatgaaattc 3960
cttcgtggca ggaaaaggtt caacatccat ctgacatgga agtttctggg gttgatagtg 4020
gatcaaaaga gcagctaagg gactgttcaa actctggaat tgaaagattt aatttcttag 4080
agaagagtat tcaaaattta gaagaggaag tattatcatc acaagattct tttgatccgg 4140
cgatatttca gtcgtgtggg agagttggat cctgttcatg ttccaaatca gacgcagagt 4200
ttcctacaac caggtgtgaa acaaaaactg tcagtggaac atcacaatca gtgcaaactg 4260
ggagcccaaa cttgtctgat gaaatttgtc ttcaagggaa tgagagaccg catctatatg 4320
aaggatctgg tgatgttcag aaacaagaaa ctacaaatgt cgctcagaag aaacctgatc 4380
ttgaaaaaac aatgaattgg aaagactctg tctgttttgg tcagccaaga aatgatacta 4440
attggcaaac aactccttcc agcagctatg agcagtgtgc gactcgacag ccacatgtac 4500
tagacataga ggattttgga atgcaaggtg aaggccttgg ttattcttgg atgtccatct 4560
caccaagagt tgacagagta aagaacaaaa atgtaccacg caggtttttc agacaaggtg 4620
gaagtgttcc aagagaattc acaggtcaga tcataccatc aacgcctcat gaattaccag 4680
gaatgggatt gtccggttcc tcaagcgccg tccaagaaca ccaggacgat acccaacata 4740
atcaacaaga tgagatgaat aaagcatccc atttacaaaa aacatttttg gatctgctca 4800
actcctctga agaatgcctt acaagacagt ccagtaccaa acagaacatc acggatggct 4860
gtctaccgag agatagaact gctgaagacg tggttgatcc gctcagtaac aattcaagct 4920
tacagaacat attggtcgaa tcaaattcca gcaataaaga gcagacggca gttgaataca 4980
aggagacaaa tgccactatt ttacgagaga tgaaagggac gcttgctgat gggaaaaagc 5040
ctacaagcca gtgggatagt ctcagaaaag atgtggaggg gaatgaaggg agacaggaac 5100
gaaacaaaaa caatatggat tccatagact atgaagcaat aagacgtgct agtatcagcg 5160
agatttctga ggctatcaag gaaagaggga tgaataacat gttggccgta cgaattaagg 5220
atttcctaga acggatagtt aaagatcatg gtggtatcga ccttgaatgg ttgagagaat 5280
ctcctcctga taaagccaag gactatctct tgagcataag aggtctgggt ttgaaaagtg 5340
ttgaatgcgt gcgactctta acactccaca atcttgcttt ccctgttgac acgaatgttg 5400
gaaggatagc agttaggatg ggatgggtgc ctctacaacc cctacctgaa tcacttcagt 5460
tacacctcct ggagctatac ccagtgctcg agtccatcca aaaatttctt ggccaagac 5520
tttgcaaact cgatcaacga acactgtatg aattacacta ccaactgatt acgtttggaa 5580
aggtattttg cacaaagagt agaccaaatt gtaatgcatg tccaatgaga ggagagtgca 5640
gacactttgc cagtgcttat gctagtgcaa gacttgcttt accggcacca gaggagagga 5700
gcttaacaag tgcaactatt ccggtccctc ccgagtcctt tcctcctgta gccatcccga 5760
tgatagaact acctcttccg ttggagaaat ccctagcaag tggagcacca tcgaatagag 5820
aaaactgtga accaataatt gaagagccgg cctcgcccgg gcaagagtgc actgaaataa 5880
ccgagagtga tattgaagat gcttactaca atgaggaccc tgacgagatc ccaacaataa 5940
aactcaacat tgaacagttt ggaatgactc tacgggaaca catggaaaga aacatggagc 6000
tccaagaagg tgacatgtcc aaggctttgg ttgctttgca tccaacaact acttctattc 6060
caactcccaa actaaagaac attagccgtc tcaggacaga gcaccaagtg tacgagctcc 6120
cagattcaca tcgtctcctt gatggtatgg ataaaagaga accagatgat ccaagtcctt 6180
atctcttagc tatatggaca ccaggtgaaa cagcgaattc ggcacaaccg cctgaacaga 6240
agtgtggagg gaaagcgtct ggcaaaatgt gctttgacga gacttgttct gagtgtaaca 6300
gtctgaggga agcaaactca cagacagttc gaggaactct tctgatacct tgtcggactg 6360
ccatgagagg aagtttttccg ctcaacggga catatttcca agtcaacgag ttatttgcag 6420
accacgagtc cagtctcaaa cccatcgatg ttcctagaga ttggatatgg gatctcccaa 6480
gaaggactgt ttacttcgga acatcagtaa catcaatatt cagaggtctt tcaacggagc 6540
agatacagtt ctgctttttgg aaaggattcg tatgtgtccg tggattcgaa cagaagacaa 6600
gagcaccgcg tccattaatg gcaaggttgc attttcctgc gagcaaattg aagaacaaca 6660
aaacctaaag atgactggaa gaaagcaaac gcattgcttc tctgctctcc tctatttaaa 6720
gccaggaaaa gtcccatttta gacataataa caggaatcca aataggctat tttctctttc 6780
```

13

```
tttcttattt cattcataga gcagaagcga cacaaaaaag ttttttgggt tatttatttt 6840
ctctctaaca aaaaaaaaa aaaaaaactc gag                                 6873


<210> 6
<211> 1478
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT 5' untranslated region

<400> 6
gttctccggc attgactcgc ctgagaatca gaaagcttag atcggtgagc ttttagctcc 60
attttctgtt tatttacata ttatttcctt tttttctctc tcccttttt atctggaatt 120
tgttctgcta aattttccag ctgttacatt ttccgatcac gagaagaatc actgggtttt 180
tatgttaatc aatacatgtt cctgtttttct gatcataaat ctcagctatt aacacctgat 240
tttgattctg cgtaataaaa acctctgatt tgctttttatc ttcactttcc ccataaacat 300
tgcttacttt attcgctctt cttttaccgt ttccagctaa aaaattcttc gctattcaat 360
gtgtttctcg ttttgttgat gagaaaaata tctgacaaaa aatcatttat tgcattttat 420
ggtgcagatt cttagttaat gtcgccttct ctaaccaagt cagattaaaa aggagtgttc 480
gtccatgttg ctttgttttg gtgtttggag agagtttttcg gagagttagg tgagtgttat 540
ttggggtgag gtagtgataa ggtttgaagg gggagtgatt catcaagtgt gttatgaatt 600
cgagggctga tccggggggat agatattttc gagttccttt ggagaatcaa actcaacaag 660
agttcatggg ttcttggatt ccatttacac ccaaaaaacc tagatcaagt ctgatggtag 720
atgagagagt gataaaccag gatctaaatg ggtttccagg tggtgaattt gtagacaggg 780
gattctgcaa cactggtgtg gatcataatg gggttttttga tcatggtgct catcagggcg 840
ttaccaactt aagtatgatg atcaatagct tagcgggatc acatgcacaa gcttggagta 900
atagtgagag agatctttttg ggcaggagtg aggtgacttc tcctttagca ccagttatca 960
gaaacaccac cggtaatgta gagccggtca atggaaattt tacttcagat gtgggtatgg 1020
taaatggtcc tttcacccag agtggcactt ctcaagctgg ctataatgag tttgaattgg 1080
atgacttgtt gaatcctgat cagatgccct tctccttcac aagcttgctg agtggtgggg 1140
atagcttatt caaggttcgt caatgtgagt gatcaaatct attttcagtt ttttttttttc 1200
cctttcttcc gttcttgcag tacttagagt agaacatgaa ttagaatatc ttaagaaagt 1260
catggttttg aacagatgga cctccagcgt gtaacaagcc tctttacaat ttgaattcac 1320
caattagaag agaagcagtt gggtcagtct gtgaaagttc gtttcaatat gtaccgtcaa 1380
cgcccagtct gttcagaaca ggtgaaaaga ctggattcct tgaacagata gttacaacta 1440
ctggacatga aatcccagag ccgaaatctg acaaaagt                          1478


<210> 7
<211> 10620
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT1 (1DMT5) gene sequence from BAC T32M21

<400> 7
tcactagatt ccaaaacgta gaccaattgt atctaatctc aaattctcaa tcaaagtatt 60
aatttaccga tggtaagaaa agttaaccga tataattatc aaaagaaaga ataagtcaac 120
agattcttaa tctctttatt ttggtatatg aacatttgta caaaaatctc aaaagatatg 180
taactgtttta aaatataaat tcactgagat taattcttca gactcgtgtt agctataata 240
atgtcaagag ttcttcttgt ttcaaggaaa aaccttaaag atatgtatat tttctgtaat 300
tatgatgata taatttgcta ttcattgtca caaacattac tttaaaaaat cgtattttca 360
ttactacaat gttgactaag aacaaaaata cattgattat tgatatatcg tcaactgaat 420
tttcttccga gggatataat tctcaaacat agcaagaatc tcataataat gtttcgtgac 480
tacctttaga cgaaattttt ttaagattcg taacgtgact tatggtctct tgctgtgggg 540
gtcaatgcga ataaatctaa atgtatggga gtcaaataaa ataccaagaa aaataaagga 600
gcagcaccca ataaactata tgggaccaga aatcctttca ttggtttaaa ataggattat 660
cccgaaagat gaaggactaa attgaaactg attggggggta ggaagagatc cgtcacaatc 720
```

14

```
attaatggct tccacgcgga aacttgtcgt ttatacaatt tcattaactt tcgggtcggg 780
tttatattcc aaatgggtca aataatatta gtttaataca ctaacggagt aattaattgg 840
tgactacaat tttatcagtt tggtgcaatt agaaacgaac atagtcgtaa aatacgagtt 900
cggtgttata cctttatta cgttaaaaaa atacgagaat tttgtgtcaa atttcaaatt 960
aatttcatga atatatggaa attattagat actctagcga aaatagtgat tatgagcgtt 1020
ttacaaaaat acgattttag cattgaactt cctttatgta attcggtcaa atgttggcat 1080
gaagaagcaa gtttgcaaca ttaaatttca tttaaaaatc gtgttgacat actttaaaat 1140
ctaaatatag gaagaagacc aaaacattaa atttagtaag attctaatga acatttataa 1200
gttataactt ataaccaaca aaagttgggt ttagcgttgt tgctttatct gaaaacttgc 1260
aaactaaacc attttaatag gactaatgac aattaacaac aaaatacact taagcaacaa 1320
cgtcctcgtg aatataattt gggcctcagg cccatattgc taacgccaac tgatatttca 1380
ctttattcct tcttcatctc accacactct ctctctatct ctatctctaa cggcatagct 1440
gactcagtgt tctccggcat tgactcgcct gagaatcaga aagcttagat cggtgagctt 1500
ttagctccat tttctgttta tttacatatt atttcctttt tttctctctc cctttttat 1560
ctggaatttg ttctgctaaa ttttccagct gttacatttt ccgatcacga gaagaatcac 1620
tgggttttta tgttaatcaa tacatgttcc tgttttctga tcataaatct cagctattaa 1680
cacctgattt tgattctgcg taataaaaac ctctgatttg cttttatctt cactttcccc 1740
ataaacattg cttactttat tcgctcttct tttaccgttt ccagctaaaa aattcttcgc 1800
tattcaatgt gtttctcgtt ttgttgatga gaaaaatatc tgacaaaaaa tcatttattg 1860
cattttatgg tgcagattct tagttaatgt cgccttctct aaccaagtca gattaaaaag 1920
gagtgttcgt ccatgttgct ttgtttttggt gtttggagag agttttcgga gagttaggtg 1980
agtgttattt ggggtgaggt agtgataagg tttgaagggg gagtgattca tcaagtgtgt 2040
tatgaattcg agggctgatc cgggggatag atattttcga gttcctttgg agaatcaaac 2100
tcaacaagag ttcatgggtt cttggattcc atttacaccc aaaaaaccta gatcaagtct 2160
gatggtagat gagagagtga taaaccagga tctaaatggg tttccaggtg gtgaatttgt 2220
agacagggga ttctgcaaca ctggtgtgga tcataatggg gtttttgatc atggtgctca 2280
tcagggcgtt accaacttaa gtatgatgat caatagctta gcgggatcac atgcacaagc 2340
ttggagtaat agtgagagag atcttttggg caggagtgag gtgacttctc ctttagcacc 2400
agttatcaga aacaccaccg gtaatgtaga gccggtcaat ggaaatttta cttcagatgt 2460
gggtatggta aatggtcctt tcacccagag tggcacttct caagctggct ataatgagtt 2520
tgaattggat gacttgttga tcctgatca gatgcccttc tccttcacaa gcttgctgag 2580
tggtggggat agcttattca aggttcgtca atgtgagtga tcaaatctat tttcagtttt 2640
ttttttcccc tttcttccgt tcttgcagta cttagagtag aacatgaatt agaatatctt 2700
aagaaagtca tggttttgaa cagatggacc tccagcgtgt aacaagcctc tttacaattt 2760
gaattcacca attagaagag aagcagttgg gtcagtctgt gaaagttcgt ttcaatatgt 2820
accgtcaacg cccagtctgt tcagaacagg tgaaagact ggattccttg aacagatagt 2880
tacaactact ggacatgaaa tcccagagcc gaaatctgac aaaagtatgc agagcattat 2940
ggactcgtct gctgttaatg cgacggaagc tactgaacaa aatgatggca gcagacaaga 3000
tgttctggag ttcgacctta acaaaactcc tcagcagaaa ccctccaaaa ggaaaaggaa 3060
gttcatgccc aaggtggtcg tggaaggcaa acctaaaaga aagccacgca aacctgcaga 3120
acttcccaaa gtggtcgtgg aaggcaaacc taaaaggaag ccacgcaaag ctgcaactca 3180
ggaaaaagtg aaatctaaag aaaccgggag tgccaaaaag aaaaatttga aagaatcagc 3240
aactaaaaag ccagccaatg ttggagatat gagcaacaaa agccctgaag tcacactcaa 3300
aagttgcaga aaagctttga attttgactt ggagaatcct ggagatgcga ggcaaggtga 3360
ctctgagtct gaaattgtcc agaacagtag tggcgcaaac tcgttttctg agatcagaga 3420
tgccattggt ggaactaatg gtagtttcct ggattcagtg tcacaaatag acaagaccaa 3480
tggattgggg gctatgaacc agccacttga agtgtcaatg ggaaaccagc cagataaact 3540
atctacagga gcgaaactgg ccagagacca acaacctgat ttattgacta gaaaccagca 3600
atgccagttc ccagtggcaa cccagaacac ccagttccca atggaaaacc aacaagcttg 3660
gcttcagatg aaaaaccaac ttattggctt tccatttggt aaccagcaac ctcgcatgac 3720
cataagaaac cagcagcctt gcttggccat gggtaatcaa caacctatgt atctgatagg 3780
aactccacgg cctgcattag taagtggaaa ccagcaacta ggaggtcccc aaggaaacaa 3840
gcggcctata tttttgaatc accagacttg tttacctgct ggaaatcagc tatatggatc 3900
acctacagac atgcatcaac ttgttatgtc aaccggaggg caacaacatg gactactgat 3960
aaaaaaccag caacctggat cattaataag aggccagcag ccttgcgtac cttttgattga 4020
ccagcaacct gcaactccaa aaggttttac tcacttgaat cagatggtag ctaccagcat 4080
gtcatcgcct gggcttcgac ctcattctca gtcacaagtt cctacaacat atctacatgt 4140
ggaatctgtt ccaggattt tgaatgggac tacaggtaca tgccagagaa gcagggctcc 4200
tgcatacgat tctttacagc aagatatcca tcaaggaaat aagtacatac tttctcatga 4260
gatatccaat ggtaatgggt gcaagaaagc gttacctcaa aactcttctc tgccaactcc 4320
aattatggct aaacttgagg aagccagggg ctcgaagaga cagtatcatc gtgcaatggg 4380
```

15

```
acagacggaa aagcatgatc taaacttagc tcaacagatt gctcaatcac aagatgtgga 4440
gagacataac agcagcacgt gtgtggaata tttagatgct gcaaagaaaa cgaaaatcca 4500
gaaagtagtc caagaaaatt tgcatggcat gccacctgag gttatagaaa tcgaggatga 4560
tccaactgat ggggcaagaa aaggtaaaaa tactgccagc atcagtaaag gtgcatctaa 4620
aggaaactcg tctccagtta aaaagacagc agaaaaggag aaatgtattg tcccaaaaac 4680
gcctgcaaaa aagggtcgag caggtagaaa aaaatcagta cctccgcctg ctcatgcctc 4740
agagatccag ctttggcaac ctactcctcc aaagacacct ttatcaagaa gcaagcctaa 4800
aggaaaaggg agaaagtcca tacaagattc aggaaaagca agaggtaact aatgtattct 4860
acaatctctg tgatataatt ttgagatttt agtaactgat gtgtccaaac cagctcctta 4920
tcactgttgg tgcgttgtat aggtccatca ggagaacttc tgtgtcagga ttctattgcg 4980
gaaataattt acaggatgca aaatctgtat ctaggagaca aagaaagaga acaagagcaa 5040
aatgcaatgg tcttgtacaa aggagatggt gcacttgttc cctatgagag caagaagcga 5100
aaaccaagac ccaaagttga cattgacgat gaaacaactc gcatatggaa cttactgatg 5160
gggaaggag atgaaaaaga aggggatgaa gagaaggata aaaagaaaga gaagtggtgg 5220
gaagaagaaa gaagagtctt ccgaggaagg gctgattcct tcatcgctcg catgcacctg 5280
gtacaaggtg aagatccact tctcttctca actccatttt tattcacaca aattagtaga 5340
atactcaaaa atgatgtttt gtttgcaaaa ttttaaaatt cactagttaa ccatgtcaaa 5400
taatattcat aatgcatctt gtgaagaaca ggtgtgcatt tatggtgaca gctgaatggt 5460
ttatgtgcct attatttctt ttactgctat agatgaccaa ttgaacttaa acgtttacag 5520
gagatagacg tttttcgcca tggaagggat cggtggttga ttcggtcatt ggagttttcc 5580
ttacacagaa tgtctcggat cacctttcaa ggtatatgag ttgccttaat aaattgagtt 5640
ccaaaacata gaaattaacc catggtggtt ttacaatgca gctctgcgtt catgtctcta 5700
gctgctcgat tccctccaaa attaagcagc agccgagaag atgaaaggaa tgttagaagc 5760
gtagttgttg aagatccaga aggatgcatt ctgaacttaa atgaaattcc ttcgtggcag 5820
gaaaaggttc aacatccatc tgacatggaa gtttctgggg ttgatagtgg atcaaaagag 5880
cagctaaggg actgttcaaa ctctggaatt gaaagattta atttcttaga gaagagtatt 5940
caaaatttag aagaggaagt attatcatca caagattctt ttgatccggc gatatttcag 6000
tcgtgtggga gagttggatc ctgttcatgt tccaaatcag acgcagagtt tcctacaacc 6060
aggtgtgaaa caaaaactgt cagtggaaca tcacaatcag tgcaaactgg gagcccaaac 6120
ttgtctgatg aaatttgtct tcaagggaat gagagaccgc atctatatga aggatctggt 6180
gatgttcaga aacaagaaac tacaaatgtc gctcagaaga aacctgatct tgaaaaaaca 6240
atgaattgga aagactctgt ctgttttggt cagccaagaa atgatactaa ttggcaaaca 6300
actccttcca gcagctatga gcagtgtgcg actcgacagc cacatgtact agacatagag 6360
gattttggaa tgcaaggtga aggccttggt tattcttgga tgtccatctc accaagagtt 6420
gacagagtaa agaacaaaaa tgtaccacgc aggttttca gacaaggtgg aagtgttcca 6480
agagaattca caggtcagat cataccatca acgcctcatg aattaccagg aatgggattg 6540
tccggttcct caagcgccgt ccaagaacac caggacgata cccaacataa tcaacaagat 6600
gagatgaata aagcatccca tttacaaaaa acatttttgg atctgctcaa ctcctctgaa 6660
gaatgcctta caagacagtc cagtaccaaa cagaacatca cggatggctg tctaccgaga 6720
gatagaactg ctgaagacgt ggttgatccg ctcagtaaca attcaagctt acagaacata 6780
ttggtcgaat caaattccag caataaagag cagacggcag ttgaatacaa ggagacaaat 6840
gccactattt tacgagagat gaaagggacg cttgctgatg ggaaaaagcc tacaagccag 6900
tgggatagtc tcagaaaaga tgtggagggg aatgaaggga gacaggaacg aaacaaaaac 6960
aatatggatt ccatagacta tgaagcaata agacgtgcta gtatcagcga gatttctgag 7020
gctatcaagg aaagagggat gaataacatg ttggccgtac gaattaaggt aaatctacta 7080
atttcagttg agaccctcat caaatctgtc agaaggcttg aacatcagta aattatgtaa 7140
ccatatttac aacattgcag gatttcctag aacggatagt taaagatcat ggtggtatcg 7200
accttgaatg gttgagagaa tctcctcctg ataaagccaa gtgggtaaat cacatttta 7260
gtgactgcaa cactagcacg atcgatttac tcaacaatta cgtcaaactg agtattaaca 7320
agttgctcat gaacatttca cagggactat ctcttgagca taagaggtct gggtttgaaa 7380
agtgttgaat gcgtgcgact cttaacactc cacaatcttg ctttccctgt gagtcagact 7440
attccattat ctactaaaaa cttagaataa ctccggctaa ctaagctgga acttgtattg 7500
atgatatgaa ggttgacacg aatgttggaa ggatagcagt taggatggga tgggtgcctc 7560
tacaacccct acctgaatca cttcagttac acctcctgga gctgtaagtt tctttttgtt 7620
tgtcatctaa acaacgaaat ttttatgcaa gtcataacca tgctgtgttt tcacagatac 7680
ccagtgctcg agtccatcca aaaatttctt tggccaagac tttgcaaact cgatcaacga 7740
acactgtatg ctcataaact ctaacaaatc atctgtctga aaaaccaata tttctttggt 7800
agaattctat tgtcattact cattactaac agcgaaatta attaacgttc tttttcttac 7860
tcaggtatga attacactac caactgatta cgtttggaaa ggtattattg ctctaagctt 7920
tgaatttatc atatggtaat ttcaagcatt gtaggcacct gatcaattat gtgtctaaat 7980
catgtgaatt catgtcaggt attttgcaca aagagtagac caaattgtaa tgcatgtcca 8040
```

16

```
atgagaggag agtgcagaca ctttgccagt gcttatgcta ggtaagcaag cttcatgta  8100
cttatatgca ataattaaag ataaaattta ggattatggg taagtaacaa aaaattaggc  8160
tcagtttcat ggtagctagc tggaaatagt attacaagaa caacataaag atcaaagaca  8220
gaatcatgga tccatatgca ctatcatttt agctcttgta atccatacat gaacactata  8280
tgccaaagta gggatttcaa atatgagatt cgatgactga tgccattgta acagtgcaag  8340
acttgcttta ccggcaccag aggagaggag cttaacaagt gcaactattc cggtccctcc  8400
cgagtcctat cctcctgtag ccatcccgat gatagaacta cctcttccgt tggagaaatc  8460
cctagcaagt ggagcaccat cgaatagaga aaactgtgaa ccaataattg aagagccggc  8520
ctcgcccggg caagagtgca ctgaaataac cgagagtgat attgaagatg cttactacaa  8580
tgaggaccct gacgagatcc caacaataaa actcaacatt gaacagtttg gaatgactct  8640
acgggaacac atggaagaa acatggagct ccaagaaggt gacatgtcca aggctttggt  8700
tgctttgcat ccaacaacta cttctattcc aactcccaaa ctaaagaaca ttagccgtct  8760
caggacagag caccaagtgt aagctaatat ctcctcctat attttatctt ccatataaat  8820
tttgggggaaa aaatcgctct ccatctggtt ttagaacatg cgggtcagcc agggttatgg  8880
catttttata tatttcaccg atcggcccga gctggctctg gttgactcgt atgccaccct  8940
gcattgaaca aaccagtagg agacaagcaa gcaaacgtt ttaagataag gtctatggta  9000
aaatgacaag gtaactgata aatgtgtcgt ctatttgcag gtacgagctc ccagattcac  9060
atcgtctcct tgatggtgta agtcaatttt taactctctc tatactcgag ttgtttcact  9120
tgagcaacac tgtttaaaag tcctcatttg ataaaataac agatggataa aagagaacca  9180
gatgatccaa gtccttatct cttagctata tggacaccag gtgagaataa aactgcaatg  9240
tttcattcat gtgtctacag tatcaaagaa agtacagcta gagctaaaaa gcatttgaaa  9300
tagagtcggt taaatatgaa agtttgaatc tgtaaatgaa agccggaacg tagcattggt  9360
ggatgttata tgtaaattag tttttgagat tggtctaatg tagttgtttg actgccaggt  9420
gaaacagcga attcggcaca accgcctgaa cagaagtgtg gagggaaagc gtctggcaaa  9480
atgtgctttg acgagacttg ttctgagtgt aacagtctga gggaagcaaa ctcacagaca  9540
gttcgaggaa ctcttctggt gagattatct tgatctttg tgttgctcat gaaaaggaga  9600
agtgagaata caagtttgct aatatcattt tttcgtcatt cacagatacc ttgtcggact  9660
gccatgagag gaagttttcc gctcaacggg acatatttcc aagtcaacga ggttagatga  9720
aataaaactc aaacagacag acgaaacatt atttctgttt agtgttggtt ctttatcctc  9780
cttgccattt tttatcttgc agttatttgc agaccacgag tccagtctca aacccatcga  9840
tgttcctaga gattggatat gggatctccc aagaaggact gtttacttcg gaacatcagt  9900
aacatcaata ttcagaggta aaaacattcg taatagagtt agttaatcaa atgtccaaaa  9960
cacaagaaag cttcaccgtc caatacacaa gaaagcttca ccttctcttt gccaaaaaag 10020
atcttagaat gttttgctga atttgtgcag gtctttcaac ggagcagata cagttctgct 10080
tttggaaagg taaacgttaa ctttcgaccc agagaaatcc ggaaaatcta ttgctttgtt 10140
ctgatcaata cgttaaacat atacacacac actttacact taggaccaat actgttctga 10200
tctgtgatag aaactggtaa acatctaaca attatgattg caggattcgt atgtgtccgt 10260
ggattcgaac agaagacaag agcaccgcgt ccattaatgg caaggttgca ttttcctgcg 10320
agcaaattga agaacaacaa aacctaaaga tgactggaag aaagcaaacg cattgcttct 10380
ctgctctcct ctatttaaag ccaggaaaag tcccatttag acataataac aggaatccaa 10440
ataggctatt ttctctttct ttcttatttc attcatagag cagaagcgac acaaaaaagt 10500
ttttggggtt atttattttc tctctaacaa atttgtagcg ttttgggtct ttttctggct 10560
gtcactagcg tggcaaatcc aatgtctgcg cacacttagg cgcattgtca ataaaatttc 10620
```

<210> 8
<211> 1413
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DMT2 (1DMT2)

<400> 8
Met Glu Lys Gln Arg Arg Glu Glu Ser Ser Phe Gln Gln Pro Pro Trp
1   5   10   15

Ile Pro Gln Thr Pro Met Lys Pro Phe Ser Pro Ile Cys Pro Tyr Thr
            20   25   30

17

```
Val Glu Asp Gln Tyr His Ser Ser Gln Leu Glu Glu Arg Arg Phe Val
        35                  40                  45

Gly Asn Lys Asp Met Ser Gly Leu Asp His Leu Ser Phe Gly Asp Leu
        50                  55                  60

Leu Ala Leu Ala Asn Thr Ala Ser Leu Ile Phe Ser Gly Gln Thr Pro
65                  70                  75                      80

Ile Pro Thr Arg Asn Thr Glu Val Met Gln Lys Gly Thr Glu Glu Val
                85                  90                  95

Glu Ser Leu Ser Ser Val Ser Asn Asn Val Ala Glu Gln Ile Leu Lys
            100             105                 110

Thr Pro Glu Lys Pro Lys Arg Lys Lys His Arg Pro Lys Val Arg Arg
        115                 120                 125

Glu Ala Lys Pro Lys Arg Glu Pro Lys Pro Arg Ala Pro Arg Lys Ser
    130                 135                 140

Val Val Thr Asp Gly Gln Glu Ser Lys Thr Pro Lys Arg Lys Tyr Val
145                 150                 155                 160

Arg Lys Lys Val Glu Val Ser Lys Asp Gln Asp Ala Thr Pro Val Glu
                165                 170                 175

Ser Ser Ala Ala Val Glu Thr Ser Thr Arg Pro Lys Arg Leu Cys Arg
            180                 185                 190

Arg Val Leu Asp Phe Glu Ala Glu Asn Gly Glu Asn Gln Thr Asn Gly
        195                 200                 205

Asp Ile Arg Glu Ala Gly Glu Met Glu Ser Ala Leu Gln Glu Lys Gln
    210                 215                 220

Leu Asp Ser Gly Asn Gln Glu Leu Lys Asp Cys Leu Leu Ser Ala Pro
225                 230                 235                 240

Ser Thr Pro Lys Arg Lys Arg Ser Gln Gly Lys Arg Lys Gly Val Gln
                245                 250                 255

Pro Lys Lys Asn Gly Ser Asn Leu Glu Glu Val Asp Ile Ser Met Ala
            260                 265                 270

Gln Ala Ala Lys Arg Arg Gln Gly Pro Thr Cys Cys Asp Met Asn Leu
    275                 280                 285

Ser Gly Ile Gln Tyr Asp Glu Gln Cys Asp Tyr Gln Lys Met His Trp
    290                 295                 300

Leu Tyr Ser Pro Asn Leu Gln Gln Gly Gly Met Arg Tyr Asp Ala Ile
305                 310                 315                 320

Cys Ser Lys Val Phe Ser Gly Gln Gln His Asn Tyr Val Ser Ala Phe
            325                 330                 335

His Ala Thr Cys Tyr Ser Ser Thr Ser Gln Leu Ser Ala Asn Arg Val
            340                 345                 350
```

18

```
Leu Thr Val Glu Glu Arg Arg Glu Gly Ile Phe Gln Gly Arg Gln Glu
        355              360              365

Ser Glu Leu Asn Val Leu Ser Asp Lys Ile Asp Thr Pro Ile Lys Lys
    370              375              380

Lys Thr Thr Gly His Ala Arg Phe Arg Asn Leu Ser Ser Met Asn Lys
385              390              395              400

Leu Val Glu Val Pro Glu His Leu Thr Ser Gly Tyr Cys Ser Lys Pro
            405              410              415

Gln Gln Asn Asn Lys Ile Leu Val Asp Thr Arg Val Thr Val Ser Lys
        420              425              430

Lys Lys Pro Thr Lys Ser Glu Lys Ser Gln Thr Lys Gln Lys Asn Leu
        435              440              445

Leu Pro Asn Leu Cys Arg Phe Pro Pro Ser Phe Thr Gly Leu Ser Pro
    450              455              460

Asp Glu Leu Trp Lys Arg Arg Asn Ser Ile Glu Thr Ile Ser Glu Leu
465              470              475              480

Leu Arg Leu Leu Asp Ile Asn Arg Glu His Ser Glu Thr Ala Leu Val
            485              490              495

Pro Tyr Thr Met Asn Ser Gln Ile Val Leu Phe Gly Gly Gly Ala Gly
            500              505              510

Ala Ile Val Pro Val Thr Pro Val Lys Lys Pro Arg Pro Arg Pro Lys
            515              520              525

Val Asp Leu Asp Asp Glu Thr Asp Arg Val Trp Lys Leu Leu Leu Glu
    530              535              540

Asn Ile Asn Ser Glu Gly Val Asp Gly Ser Asp Glu Gln Lys Ala Lys
545              550              555              560

Trp Trp Glu Glu Glu Arg Asn Val Phe Arg Gly Arg Ala Asp Ser Phe
            565              570              575

Ile Ala Arg Met His Leu Val Gln Gly Asp Arg Arg Phe Thr Pro Trp
            580              585              590

Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr Gln Asn
    595              600              605

Val Ser Asp His Leu Ser Ser Ser Ala Phe Met Ser Leu Ala Ser Gln
    610              615              620

Phe Pro Val Pro Phe Val Pro Ser Ser Asn Phe Asp Ala Gly Thr Ser
625              630              635              640

Ser Met Pro Ser Ile Gln Ile Thr Tyr Leu Asp Ser Glu Glu Thr Met
            645              650              655

Ser Ser Pro Pro Asp His Asn His Ser Ser Val Thr Leu Lys Asn Thr
            660              665              670
```

19

```
Gln Pro Asp Glu Glu Lys Asp Tyr Val Pro Ser Asn Glu Thr Ser Arg
        675                 680             685

Ser Ser Ser Glu Ile Ala Ile Ser Ala His Glu Ser Val Asp Lys Thr
        690             695             700

Thr Asp Ser Lys Glu Tyr Val Asp Ser Asp Arg Lys Gly Ser Ser Val
705             710                 715                 720

Glu Val Asp Lys Thr Asp Glu Lys Cys Arg Val Leu Asn Leu Phe Pro
            725             730                 735

Ser Glu Asp Ser Ala Leu Thr Cys Gln His Ser Met Val Ser Asp Ala
            740             745                 750

Pro Gln Asn Thr Glu Arg Ala Gly Ser Ser Ser Glu Ile Asp Leu Glu
        755             760                 765

Gly Glu Tyr Arg Thr Ser Phe Met Lys Leu Leu Gln Gly Val Gln Val
770             775                 780

Ser Leu Glu Asp Ser Asn Gln Val Ser Pro Asn Met Ser Pro Gly Asp
785             790                 795                 800

Cys Ser Ser Glu Ile Lys Gly Phe Gln Ser Met Lys Glu Pro Thr Lys
            805             810                 815

Ser Ser Val Asp Ser Ser Glu Pro Gly Cys Cys Ser Gln Gln Asp Gly
            820             825                 830

Asp Val Leu Ser Cys Gln Lys Pro Thr Leu Lys Glu Lys Gly Lys Lys
        835             840                 845

Val Leu Lys Glu Glu Lys Lys Ala Phe Asp Trp Asp Cys Leu Arg Arg
        850             855                 860

Glu Ala Gln Ala Arg Ala Gly Ile Arg Glu Lys Thr Arg Ser Thr Met
865             870                 875                 880

Asp Thr Val Asp Trp Lys Ala Ile Arg Ala Ala Asp Val Lys Glu Val
            885             890                 895

Ala Glu Thr Ile Lys Ser Arg Gly Met Asn His Lys Leu Ala Glu Arg
            900             905                 910

Ile Gln Tyr Leu Thr Leu Asn Met Lys Ile Met Gln Gly Phe Leu Asp
        915             920                 925

Arg Leu Val Asn Asp His Gly Ser Ile Asp Leu Glu Trp Leu Arg Asp
        930             935                 940

Val Pro Pro Asp Lys Ala Lys Glu Tyr Leu Leu Ser Phe Asn Gly Leu
945             950                 955                 960

Gly Leu Lys Ser Val Glu Cys Val Arg Leu Leu Thr Leu His His Leu
            965             970                 975

Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile Ala Val Arg Leu Gly
        980             985                 990
```

20

Trp Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu His Leu Leu
    995   1000   1005

Glu Met Tyr Pro Met Leu Glu Ser Ile Gln Lys Tyr Leu Trp Pro Arg
   1010   1015   1020

Leu Cys Lys Leu Asp Gln Lys Thr Leu Tyr Glu Leu His Tyr Gln Met
1025   1030   1035   1040

Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Lys Pro Asn Cys Asn
         1045   1050   1055

Ala Cys Pro Met Lys Gly Glu Cys Arg His Phe Ala Ser Ala Phe Ala
       1060   1065   1070

Arg Lys Phe Ser Asn Ile His Leu Phe Tyr Ser Ala Arg Leu Ala Leu
    1075   1080   1085

Pro Ser Thr Glu Lys Gly Met Gly Thr Pro Asp Lys Asn Pro Leu Pro
    1090   1095   1100

Leu His Leu Pro Glu Pro Phe Gln Arg Glu Gln Gly Ser Glu Val Val
1105   1110   1115   1120

Gln His Ser Glu Pro Ala Lys Lys Val Thr Cys Cys Glu Pro Ile Ile
       1125   1130   1135

Glu Glu Pro Ala Ser Pro Glu Pro Glu Thr Ala Glu Val Ser Ile Ala
       1140   1145   1150

Asp Ile Glu Glu Ala Phe Phe Glu Asp Pro Glu Glu Ile Pro Thr Ile
      1155   1160   1165

Arg Leu Asn Met Asp Ala Phe Thr Ser Asn Leu Lys Lys Ile Met Glu
    1170   1175   1180

His Asn Lys Glu Leu Gln Asp Gly Asn Met Ser Ser Ala Leu Val Ala
1185   1190   1195   1200

Leu Thr Ala Glu Thr Ala Ser Leu Pro Met Pro Lys Leu Lys Asn Ile
       1205   1210   1215

Ser Gln Leu Arg Thr Glu His Arg Val Tyr Glu Leu Pro Asp Glu His
      1220   1225   1230

Pro Leu Leu Ala Gln Leu Glu Lys Arg Glu Pro Asp Asp Pro Cys Ser
    1235   1240   1245

Tyr Leu Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asp Ser Ile Gln
   1250   1255   1260

Pro Ser Val Ser Thr Cys Ile Phe Gln Ala Asn Gly Met Leu Cys Asp
   1265   1270   1275   1280

Glu Glu Thr Cys Phe Ser Cys Asn Ser Ile Lys Glu Thr Arg Ser Gln
      1285   1290   1295

Ile Val Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly
    1300   1305   1310

```
Ser Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala
        1315                1320                1325

Asp His Ala Ser Ser Leu Asn Pro Ile Asn Val Pro Arg Glu Leu Ile
    1330                1335                1340

Trp Glu Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser Val Pro Thr
1345                1350                1355                1360

Ile Phe Lys Gly Leu Ser Thr Glu Lys Ile Gln Ala Cys Phe Trp Lys
            1365                1370                1375

Gly Tyr Val Cys Val Arg Gly Phe Asp Arg Lys Thr Arg Gly Pro Lys
            1380                1385                1390

Pro Leu Ile Ala Arg Leu His Phe Pro Ala Ser Lys Leu Lys Gly Gln
        1395                1400                1405

Gln Ala Asn Leu Ala
    1410


<210> 9
<211> 480
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DMT2 (1DMT2) novel amino terminus

<400> 9
Met Glu Lys Gln Arg Arg Glu Glu Ser Ser Phe Gln Gln Pro Pro Trp
  1               5                   10                  15

Ile Pro Gln Thr Pro Met Lys Pro Phe Ser Pro Ile Cys Pro Tyr Thr
            20                  25                  30

Val Glu Asp Gln Tyr His Ser Ser Gln Leu Glu Glu Arg Arg Phe Val
            35                  40                  45

Gly Asn Lys Asp Met Ser Gly Leu Asp His Leu Ser Phe Gly Asp Leu
    50                  55                  60

Leu Ala Leu Ala Asn Thr Ala Ser Leu Ile Phe Ser Gly Gln Thr Pro
65                  70                  75                  80

Ile Pro Thr Arg Asn Thr Glu Val Met Gln Lys Gly Thr Glu Glu Val
                85                  90                  95

Glu Ser Leu Ser Ser Val Ser Asn Asn Val Ala Glu Gln Ile Leu Lys
            100                 105                 110

Thr Pro Glu Lys Pro Lys Arg Lys Lys His Arg Pro Lys Val Arg Arg
        115                 120                 125

Glu Ala Lys Pro Lys Arg Glu Pro Lys Pro Arg Ala Pro Arg Lys Ser
    130                 135                 140

Val Val Thr Asp Gly Gln Glu Ser Lys Thr Pro Lys Arg Lys Tyr Val
145                 150                 155                 160


                                    22
```

```
Arg Lys Lys Val Glu Val Ser Lys Asp Gln Asp Ala Thr Pro Val Glu
            165             170             175

Ser Ser Ala Ala Val Glu Thr Ser Thr Arg Pro Lys Arg Leu Cys Arg
            180             185             190

Arg Val Leu Asp Phe Glu Ala Glu Asn Gly Glu Asn Gln Thr Asn Gly
            195             200             205

Asp Ile Arg Glu Ala Gly Glu Met Glu Ser Ala Leu Gln Glu Lys Gln
    210             215             220

Leu Asp Ser Gly Asn Gln Glu Leu Lys Asp Cys Leu Leu Ser Ala Pro
225             230             235             240

Ser Thr Pro Lys Arg Lys Arg Ser Gln Gly Lys Arg Lys Gly Val Gln
            245             250             255

Pro Lys Lys Asn Gly Ser Asn Leu Glu Glu Val Asp Ile Ser Met Ala
            260             265             270

Gln Ala Ala Lys Arg Arg Gln Gly Pro Thr Cys Cys Asp Met Asn Leu
    275             280             285

Ser Gly Ile Gln Tyr Asp Glu Gln Cys Asp Tyr Gln Lys Met His Trp
    290             295             300

Leu Tyr Ser Pro Asn Leu Gln Gln Gly Gly Met Arg Tyr Asp Ala Ile
305             310             315             320

Cys Ser Lys Val Phe Ser Gly Gln Gln His Asn Tyr Val Ser Ala Phe
            325             330             335

His Ala Thr Cys Tyr Ser Ser Thr Ser Gln Leu Ser Ala Asn Arg Val
            340             345             350

Leu Thr Val Glu Glu Arg Arg Glu Gly Ile Phe Gln Gly Arg Gln Glu
    355             360             365

Ser Glu Leu Asn Val Leu Ser Asp Lys Ile Asp Thr Pro Ile Lys Lys
    370             375             380

Lys Thr Thr Gly His Ala Arg Phe Arg Asn Leu Ser Ser Met Asn Lys
385             390             395             400

Leu Val Glu Val Pro Glu His Leu Thr Ser Gly Tyr Cys Ser Lys Pro
            405             410             415

Gln Gln Asn Asn Lys Ile Leu Val Asp Thr Arg Val Thr Val Ser Lys
            420             425             430

Lys Lys Pro Thr Lys Ser Glu Lys Ser Gln Thr Lys Gln Lys Asn Leu
            435             440             445

Leu Pro Asn Leu Cys Arg Phe Pro Pro Ser Phe Thr Gly Leu Ser Pro
    450             455             460

Asp Glu Leu Trp Lys Arg Arg Asn Ser Ile Glu Thr Ile Ser Glu Leu
465             470             475             480
```

<210> 10
<211> 8880
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT2 (1DMT2) sequence from BAC F1011

<400> 10
```
tcgctgagcc tgggtttctt catcggacct ggatctctgg atctatcaaa cggtctacga 60
ggattctcca ttccaaagaa ctatacaata caagaggtac gcaaataatg ccctaaatta 120
aacctaatcg gcaaaaatcg attgcagtga caacaaatcc tcgttagagg ggaattcaga 180
gcattacaac aatcagtaac cctaagttac aatctaaaaa ttgagatgca taacgcgatt 240
ctgcgaagaa gacggagaag atagaaggaa tgcttcgaat tcggcaaaaa tgtcagagag 300
tttggacaat ctccgatcaa ttagggttgt gaattgggga ttttatggag acgagacaaa 360
aaaaagttga agatcggagc tggttccaaa aatatttagg cccatttaat gacccacatt 420
ccatgtataa taggcccatc atctaatatt tgacaacaat agaattcttt ggtccggttg 480
aactatctga tttaaaccaa gttaagtgag atcctccaca tatcgaacca gatcttgatt 540
caggtaacca aaagctaacc gtaaattcag atataaacca aacgaaggga acagagagtt 600
tacacagcta cgggtctgtt ttttgtgaca agtgtttgat acaaatttaa gacgaaacta 660
aaatgggatt tagaaacctt gtacaactct aggactgtta actttacgtt ttcactttct 720
tacattaact agattggaac agtgtgctct ctcactctta accataagct tgtatttgtt 780
tgcttgccaa cggattaggc gaggttagct tgttgtccct tcagtttgct cgccgggaag 840
tgcaatcttg caatcaaagg cttcggtccc ctcgtctttc gatcaaatcc acgtacacat 900
acgtacccta cataatatca aaagataagt tatgtttcag aacaagaaga aactgcttaa 960
tacaaaatgt acctttccaa aagcaagcct gtatcttctc agttgataaa cctgagaaaa 1020
atagagctca agtggttaga caacttttct tttatataaa caatcgcatc acaatccaat 1080
aaagaaaatc ttataccttt gaatatcgta ggaacagagg taccaaaata gaccgttctt 1140
cgaggtaatt cccatatcaa ttcccttggg acattgattg ggtttaggct ggatgcatga 1200
tccgcaaaca cctgtatcaa tagaatacat cacaagtttc aatgcaaata attaaaatga 1260
aagagttgga gttattggag ttcaagtctt acctcatttta cttgaaagta cgttccattt 1320
agaggaaaac tacccctcat cgctgttcta caaggaatct gtacaattta caacatatta 1380
atctgtagaa aacataagtg tagtaagccg cataaggaga ttgatgcaac tacttaccaa 1440
aattgtccct ctcacaattt gagatctagt ctccttgatg ctgttgcagg agaaacaagt 1500
ctcctcgtca caaagcatac catttgcttg gaatatgcac gtactaacag acggttgaat 1560
agaatcagcc gtctcacctg ttgaataaca catcgattaa agataccgat ttgatttcat 1620
gattaaaaga tatgcaaatc attaaattac ctggcgtcca tatagcaagc aaataagaac 1680
atggatcatc aggttctctc ttttccaact gccacaagaa atcacaaaca gctagtcaga 1740
ttttacaata tagacagcac tctatacggc atgtgtcctt atccagttag ctcacatacc 1800
tgagctagaa gaggatgctc gtctggaagt tcgtaactgc aagatacggg aaaagaaaca 1860
agttatggca tagcctgtaa ttattgggaa gtttgtctgc tttccaactt acgagttcat 1920
gcttggtcaa tcacttaaat attctactct gttcaagctt taataatttt gaaaaatgtg 1980
tttctgattt catttttaac ctaagaacga agaaaaacag agaaaaatgg attcttacac 2040
tcggtgttct gtccttaact ggctgatatt cttgagctta ggcattggaa gagaagcagt 2100
ttcagcagta agtgcaacta aagcgctgga catgtttccg tcttgaagtt ccttgttgtg 2160
ttccattatc ttcttcaagt tactggtaaa tgcatccatg tttagcctga tggtaggaat 2220
ttcttctgga tcctcaaaaa acgcctcctc tatgtcagct attgatactt ctgcggtttc 2280
tggctccggt gaagcaggct cttcgatgat tggttcacaa catgtgacct tttttgctgg 2340
ttctgagtgc tgtactactt cagacccttg ctctctctgg aatggctctg gcaggtgtag 2400
aggcaaaggg ttttatcag gtgtccccat accttctct gtacttggta aagcaagcct 2460
tgcactgtaa aacaaatgaa tgttactaaa ttttctgtaa tgatgattca gagcttcgtt 2520
tagatacaga ccaattctca tttaactggg ttatatttta acaaggactt tcctcataga 2580
gtcatagtgg tactaaaggt ttaagagaac atgttgtagc accttgcaaa cgcactggca 2640
aaatgtctgc attctccttt catcggacat gcattgcaat taggtttgct ctttgtgcaa 2700
aagacctgat acaataatca agcagattac aaacctcatc atgtgagctg attttgacat 2760
acgtatatat gtatttcttt aatacatacc tttccaaaag taatcatctg gtagtgcaac 2820
tcatacctgt gagataatag ggtattaaac taatgaataa gtgtattaga ctgaggcatg 2880
aaaaaaaaaa agttagtgat aaacatcatt cttacaatgt tttttggtcg agtttgcaga 2940
gacggggcca aagatacttt tgaatagatt caagcatagg atacctagac aaaccaaacc 3000
tcagatgtat taagtaacaa attacaattt ccaagtagga ccattttgaa aagtgcttac 3060
atttccagaa gatgcaactg aagtgactct gggagcggct gaaggggcac ccatccaagt 3120
```

```
ctgacggcta tgcgcccaac atttgtatca acctgtcaat aaaattaagtt catgcatcat 3180
ataattcact tttttataggg acagaaacaa aagtttgatc cttgcttact ggaaaggcaa 3240
gatggtgaag tgttagaagc cgcacacact ccacactttt cagtcccaat ccgttaaagc 3300
tcagaagata ttctctgcag ggttttgtaa tatacgagag tacataattc attattaagt 3360
cactaaaact gccaaagtag taatctttgt ataggttaat aaagaagaaa taaaatgctt 3420
cgtctttcaa acttactttg ctttatctgg tggaacatct ctcaaccatt caagatcgat 3480
acttccatgg tcatttacca gtcgatcaag gaagccctgc atgattttca tgttcagagt 3540
caaatactta aaatgaatgt tatcacgaaa tttagccact aaattttttac ctgtatacgt 3600
tctgcaagtt tatggttcat cccgcgactc ttgattgttt cagcaacttc cttaacatct 3660
gctgctcgta ttgccttcca atccacggtg tccattgtac ttcttgtttt ttctctaatt 3720
cctgctctag cttgggcttc tcttcttaaa caatcccagt caaacgcttt ttttttcctcc 3780
ttcaaaacct ttttcccttt ttcttttaag gtaggtttct gacaactcaa aacatcccca 3840
tcttgctgag agcaacaacc aggttcacta ctatcaacag aggattttgt gggctctttc 3900
attgactgga aacccttaat ttctgagcta caatcacccg gagacatatt tggtgatact 3960
tgattggaat cttctagaga gacttgtacc ccctgtagga gcttcataaa ggaagtacga 4020
tactctcctt ctaagtcgat ctctgagctt gatcctgctc tctctgtatt ttgaggagca 4080
tcagacacca tcgaatgttg acatgtaagt gcagaatctt cagatggaaa caggttcagg 4140
acacgacact tctcatccgt cttatcaacc tctacacttg agcctttttcg atctgaatca 4200
acatactcct ttgaatccgt ggttttgtca actgattcat gggctgagat ggcaatctca 4260
ctactgcttc tggaggtttc attgctaggt acataatcct tctcctcatc aggctgtgta 4320
tttttcaaag taacagaact gtgattgtga tcgggtgggc ttgacatcgt ttcctctgag 4380
tccaagtacg ttatttgaat agaaggcatc gagcttgttc cagcgtcaaa gttactgctc 4440
ggtacaaaag ggacagggaa ctgggaagcc aacgacatga aagccgaact acaaggagta 4500
aaaaacatca aagcaagtta gttttgtgac ttttttgctgt cttggattta gtttgacata 4560
gaattatgta agagcttgta ccttgagaga tggtctgaaa catttttgagt gagaaatact 4620
ccaacaacag aatccacgac ggatcccttc caaggcgtaa aacgtcgatc ccctgttaga 4680
aaccaaagac cataacaaga agcagtagct gagacatact aattgaaacc atgtggttag 4740
aacagaaaca cataaaagga caagtgtggt gtataacctt gtacaaggtg catccttgca 4800
ataaatgagt cagctcgtcc tcgaaacaca ttacgttctt cctcccacca tttcgccttc 4860
tgctcgtctg atccgtcaac accttcgcta ttaatattct ccaatagcag tttccacact 4920
ctgtctgtct catcgtctag atcaaccttt ggtcgtgggc gtggtttttt aacaggagtt 4980
acaggcacaa ttgctccagc gccaccacca aagagtacaa tctggctatt cattgtgtaa 5040
ggaacgagag cagtttcaga atgctccctg ttgatgtcta atagacgcaa tagctcactg 5100
attgtttcga tcgagttacg tcgttccaa agttcatctg gagaaagacc tgcaggaatc 5160
aaacatcatc attatcaaga aatagtctgc atttaacaga ttcaaaaaaa caaagaaata 5220
tagttctgta tctattcatt accagtaaat gaaggtggaa aacggcaaag attcggaaga 5280
agatttttct gtttggtttg tgatttctca gacttggttg gcttcttttt gctcacagtc 5340
acccgcgtat caacaagaat cttattattt tgctgtggct tgctacaata tcctgaggtt 5400
aaatgctcag gaacttccac aagtttattc attgaagaca aattccggaa tcgagcatgg 5460
cctgttgttt tcttcttgat cggcgtgtct atcttatccg agagaacatt tagctcagac 5520
tcttgccttc cttgaaagat accttctcgt ctttcttcaa cggttaggac tctattagca 5580
ctgagctgag atgtggaact gtagcacgta gcgtgaaagg cagaaacata attgtgctgt 5640
tgtccagaga atactttgct gcaaatggca tcatatctca tccctccctg ttgcaagttt 5700
ggggaataca accaatgcat tttctggtag tcacattgct catcatactg aatccctgat 5760
agattcatgt cgcaacaagt tggtccttgt cttctctttg cagcttgcgc catcgaaata 5820
tcgacttctt ctagattact gccattttttc tttggttgaa ctcccttttct tttaccttgg 5880
ctgcgctttc tcttgggcgt gctaggagcc gaaagaaggc aatcttttaa ctcttgattc 5940
ccagaatcta actgcttctc ttgaagagct gattccatct cacctgcttc tctaatgtca 6000
ccgttggtct ggtttttctcc atttttcggct tcaaaatcca agactcgtct acagagcctc 6060
ttaggacgag ttgaagtttc aacagctgct gatgattcaa ccggagtagc gtcttgatcc 6120
ttactgactt caaccttctt ccgcacatat ttcctctttg gtgttttgct ttcttgacca 6180
tcggtgacaa cagacttcct cggagctcgt ggtttaggct ccctcttggg tttagcttct 6240
ctacgaacct ttggccgatg cttcttcctc ttaggttttt caggagtctt gaggatctgt 6300
tcagcaacat tgttactcac tgagctcaaa ctctccactt cttcagtacc tttttgcata 6360
acctctgtgt ttcctacatt gagaatcaca tctttctcag tccaactcaa acagaatcaa 6420
aatttgacaa agcgatttca tttctcatga gaccagaatc aaaatcccct cttacttgta 6480
ggtattggag tctgaccaga gaatatgagg gatgcagtgt tagctagagc aagcaaatcc 6540
ccaaaagaca agtgatcaag accactcata tccttgttcc caacaaatct cctgcatgca 6600
tcaatacctt acttaaccaa ttacccatca ctactctttg aaatttctca actttagaac 6660
aaaaaagcac aaacctttcc tccaattgac tgctatgata ttgatcctcc accgtgtatg 6720
ggcagatcgg tgaaaatggc ttcatgggtg tctgaggaat ccatggaggt tgttgaaagc 6780
```

```
tgctttcttc tctcctctgt ttctccattt ctgactctat ttttactttt cttcactctt 6840
acttaaatca gaaccatttg agaaaaagct tggaactttc tattttttcc actgcaaaaa 6900
gttcaataat ttcttcaata aaagagatca ccaatttttt ttaaaaatca cgatttata 6960
aaatgatcag atccactttt ttctgggtt ttagagaaag agagatctcc ggaagtcatt 7020
gattttgggt gagtggcgac atgaacgatt aatccgttcg ttaggtgaaa gagagacttt 7080
ttagattcac aacaaaatgt aaaaaaaagt aagaaaaaaa caaaattcat taccagtaga 7140
atcaatggtt atggtggtga tggagagagt tagttcggtg gtagctatga gaggataaga 7200
tcactgatgc ttcgtttctt ctcttggaat cgatgaagtt aaagagtaat atagaaaaag 7260
cttttttggc ctaacgtata aagaagagga tataacatgt gttgttgtgt gtttcactat 7320
ttttcataac cgtttgttta tgtagggcga aagttcgttt ggttggcggg aaaagtttta 7380
cggaatttta ttttaaaaat aatgattctt ttctacaaaa tctcctagac tatgggaaag 7440
atgatttaaa aagtaataa tattgtcgtt gttatcgtca tcgtcatcat cgtctttct 7500
gttatctttt tctctttaaa atttcgtatt ttttctcgtt tacgtaacta tttaaaatta 7560
tatgaactaa ctaattttat aattaataga aattataaaa taatcttaat tttgctttag 7620
atataaaata attagaactt tatttataaa tttatcatca aattatgatt taaacaaata 7680
acatgttatg taatccacgt ttataatttt gatcaataat atattatttt gctaattttt 7740
acgtaatctc ataaatttac acgttttcgt ttacatatgc agaagttaaa tgattcgttt 7800
tagaattatt attttccact gatatgggag ctagtgtagt agagtgatta ttaggctagt 7860
tgcccaacga gtctttcgtt tttgatcatt ccaaatgttt tagtctagta cgataggagt 7920
caaaatactg caccatatgt gtgaaactgt gaatgtgtgt gaaaaaaaga gtaattagtg 7980
tgctaacctt tgatttcctg tcatgcaaga aaccttcaaa gagacgtaca tgagaaatga 8040
gtattgtaaa tcatttattt catggacttg gttggaatct tagtgaatcg ttgttgtcaa 8100
tcttaacaac ttgttggatt ggttatgagc ctatgactta tgacttatga gtgagtcaat 8160
ggtggtcata acctaatgat tgggttatga gcaaagaaat ttggaatttg taaaaaaaaa 8220
aaaaaaaatc aagagctttt ttgtgtggac atatctatcc tagaaactga gacgaataat 8280
agtggataaa aagttgggaa cggattattc gaatgtttaa aactattatt gaaaacaata 8340
caactaaata tggtacaaaa gtaaacgaat tcgtatagct aaacctaatt caaattacga 8400
agctaatcca tacttggatc ctaaacgctt ttactttac ttacggtttc tttttcaaaa 8460
aagttttac aaatttgggt ttgtcttatg aagattatgg cagaagagac tgatcaaaag 8520
tgaatgccta attcggttta atccattcaa gtttatctta aacaatgaaa ctgaccatga 8580
aagtgaattc aaagaccaaa tcaaagaaaa attaaactga tttagttgta atattggtat 8640
tgaattaaac tataaataga aataaccaaa catataacca caaaagaaga ctatttatat 8700
aaatatatga gttggaagtc atttttggac tattatataa gatctaatta tcacacgacg 8760
tgtggatgta tggttagcag agttgtgttc agagagttcg ataaagccat cactccaaac 8820
atacaaaata tccatacatt gatccaccaa tataaccggc tgtgtgccaa gcaaagtgaa 8880
```

<210> 11
<211> 1332
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DMT3 (1DMT3)

<400> 11

```
Met Glu Val Glu Gly Glu Val Arg Glu Lys Glu Ala Arg Val Lys Gly
1               5                   10                  15

Arg Gln Pro Glu Thr Glu Val Leu His Gly Leu Pro Gln Glu Gln Ser
            20                  25                  30

Ile Phe Asn Asn Met Gln His Asn His Gln Pro Asp Ser Asp Arg Arg
        35                  40                  45

Arg Leu Ser Leu Glu Asn Leu Pro Gly Leu Tyr Asn Met Ser Cys Thr
    50                  55                  60

Gln Leu Leu Ala Leu Ala Asn Ala Thr Val Ala Thr Gly Ser Ser Ile
65                  70                  75                  80
```

26

```
Gly Ala Ser Ser Ser Ser Leu Ser Ser Gln His Pro Thr Asp Ser Trp
            85                      90                      95

Ile Asn Ser Trp Lys Met Asp Ser Asn Pro Trp Thr Leu Ser Lys Met
            100                     105                     110

Gln Lys Gln Gln Tyr Asp Val Ser Thr Pro Gln Lys Phe Leu Cys Asp
        115                 120                 125

Leu Asn Leu Thr Pro Glu Glu Leu Val Ser Thr Ser Thr Gln Arg Thr
    130                 135                 140

Glu Pro Glu Ser Pro Gln Ile Thr Leu Lys Thr Pro Gly Lys Ser Leu
145                 150                 155                 160

Ser Glu Thr Asp His Glu Pro His Asp Arg Ile Lys Lys Ser Val Leu
                165                 170                 175

Gly Thr Gly Ser Pro Ala Ala Val Lys Lys Arg Lys Ile Ala Arg Asn
            180                 185                 190

Asp Glu Lys Ser Gln Leu Glu Thr Pro Thr Leu Lys Arg Lys Lys Ile
        195                 200                 205

Arg Pro Lys Val Val Arg Glu Gly Lys Thr Lys Lys Ala Ser Ser Lys
    210                 215                 220

Ala Gly Ile Lys Lys Ser Ser Ile Ala Ala Thr Ala Thr Lys Thr Ser
225                 230                 235                 240

Glu Glu Ser Asn Tyr Val Arg Pro Lys Arg Leu Thr Arg Arg Ser Ile
                245                 250                 255

Arg Phe Asp Phe Asp Leu Gln Glu Glu Asp Glu Glu Phe Cys Gly Ile
        260                 265                 270

Asp Phe Thr Ser Ala Gly His Val Glu Gly Ser Ser Gly Glu Glu Asn
        275                 280                 285

Leu Thr Asp Thr Thr Leu Gly Met Phe Gly His Val Pro Lys Gly Arg
    290                 295                 300

Arg Gly Gln Arg Arg Ser Asn Gly Phe Lys Lys Thr Asp Asn Asp Cys
305                 310                 315                 320

Leu Ser Ser Met Leu Ser Leu Val Asn Thr Gly Pro Gly Ser Phe Met
            325                 330                 335

Glu Ser Glu Glu Asp Arg Pro Ser Asp Ser Gln Ile Ser Leu Gly Arg
        340                 345                 350

Gln Arg Ser Ile Met Ala Thr Arg Pro Arg Asn Phe Arg Ser Leu Lys
        355                 360                 365

Lys Leu Leu Gln Arg Ile Ile Pro Ser Lys Arg Asp Arg Lys Gly Cys
    370                 375                 380

Lys Leu Pro Arg Gly Leu Pro Lys Leu Thr Val Ala Ser Lys Leu Gln
385                 390                 395                 400
```

27

```
Leu Lys Val Phe Arg Lys Lys Arg Ser Gln Arg Asn Arg Val Ala Ser
            405             410             415

Gln Phe Asn Ala Arg Ile Leu Asp Leu Gln Trp Arg Arg Gln Asn Pro
            420             425             430

Thr Gly Thr Ser Leu Ala Asp Ile Trp Glu Arg Ser Leu Thr Ile Asp
            435             440             445

Ala Ile Thr Lys Leu Phe Glu Glu Leu Asp Ile Asn Lys Glu Gly Leu
    450             455             460

Cys Leu Pro His Asn Arg Glu Thr Ala Leu Ile Leu Tyr Lys Lys Ser
465             470             475             480

Tyr Glu Glu Gln Lys Ala Ile Val Lys Tyr Ser Lys Lys Gln Lys Pro
            485             490             495

Lys Val Gln Leu Asp Pro Glu Thr Ser Arg Val Trp Lys Leu Leu Met
            500             505             510

Ser Ser Ile Asp Cys Asp Gly Val Asp Gly Ser Asp Glu Glu Lys Arg
            515             520             525

Lys Trp Trp Glu Glu Glu Arg Asn Met Phe His Gly Arg Ala Asn Ser
            530             535             540

Phe Ile Ala Arg Met Arg Val Val Gln Gly Asn Arg Thr Phe Ser Pro
545             550             555             560

Trp Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr Gln
            565             570             575

Asn Val Ala Asp His Ser Ser Ser Ser Ala Tyr Met Asp Leu Ala Ala
            580             585             590

Glu Phe Pro Val Glu Trp Asn Phe Asn Lys Gly Ser Cys His Glu Glu
            595             600             605

Trp Gly Ser Ser Val Thr Gln Glu Thr Ile Leu Asn Leu Asp Pro Arg
    610             615             620

Thr Gly Val Ser Thr Pro Arg Ile Arg Asn Pro Thr Arg Val Ile Ile
625             630             635             640

Glu Glu Ile Asp Asp Asp Glu Asn Asp Ile Asp Ala Val Cys Ser Gln
            645             650             655

Glu Ser Ser Lys Thr Ser Asp Ser Ser Ile Thr Ser Ala Asp Gln Ser
            660             665             670

Lys Thr Met Leu Leu Asp Pro Phe Asn Thr Val Leu Met Asn Glu Gln
            675             680             685

Val Asp Ser Gln Met Val Lys Gly Lys Gly His Ile Pro Tyr Thr Asp
    690             695             700

Asp Leu Asn Asp Leu Ser Gln Gly Ile Ser Met Val Ser Ser Ala Ser
705             710             715             720
```

28

Thr His Cys Glu Leu Asn Leu Asn Glu Val Pro Pro Glu Val Glu Leu
              725   730   735

Cys Ser His Gln Gln Asp Pro Glu Ser Thr Ile Gln Thr Gln Asp Gln
              740   745   750

Gln Glu Ser Thr Arg Thr Glu Asp Val Lys Lys Asn Arg Lys Lys Pro
              755   760   765

Thr Thr Ser Lys Pro Lys Lys Lys Ser Lys Glu Ser Ala Lys Ser Thr
    770   775   780

Gln Lys Lys Ser Val Asp Trp Asp Ser Leu Arg Lys Glu Ala Glu Ser
785   790   795   800

Gly Gly Arg Lys Arg Glu Arg Thr Glu Arg Thr Met Asp Thr Val Asp
              805   810   815

Trp Asp Ala Leu Arg Cys Thr Asp Val His Lys Ile Ala Asn Ile Ile
              820   825   830

Ile Lys Arg Gly Met Asn Asn Met Leu Ala Glu Arg Ile Lys Ala Phe
              835   840   845

Leu Asn Arg Leu Val Lys Lys His Gly Ser Ile Asp Leu Glu Trp Leu
    850   855   860

Arg Asp Val Pro Pro Asp Lys Ala Lys Glu Tyr Leu Leu Ser Ile Asn
865   870   875   880

Gly Leu Gly Leu Lys Ser Val Glu Cys Val Arg Leu Leu Ser Leu His
              885   890   895

Gln Ile Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile Ala Val Arg
              900   905   910

Leu Gly Trp Val Pro Leu Gln Pro Leu Pro Asp Glu Leu Gln Met His
              915   920   925

Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Val Gln Lys Tyr Leu Trp
    930   935   940

Pro Arg Leu Cys Lys Leu Asp Gln Lys Thr Leu Tyr Glu Leu His Tyr
945   950   955   960

His Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Val Lys Pro Asn
              965   970   975

Cys Asn Ala Cys Pro Met Lys Ala Glu Cys Arg His Tyr Ser Ser Ala
              980   985   990

Arg Ala Ser Ala Arg Leu Ala Leu Pro Glu Pro Glu Glu Ser Asp Arg
              995   1000   1005

Thr Ser Val Met Ile His Glu Arg Arg Ser Lys Arg Lys Pro Val Val
    1010   1015   1020

Val Asn Phe Arg Pro Ser Leu Phe Leu Tyr Gln Glu Lys Glu Gln Glu
1025   1030   1035   1040

29

Ala Gln Arg Ser Gln Asn Cys Glu Pro Ile Ile Glu Glu Pro Ala Ser
        1045   1050   1055

Pro Glu Pro Glu Tyr Ile Glu His Asp Ile Glu Asp Tyr Pro Arg Asp
            1060   1065   1070

Lys Asn Asn Val Gly Thr Ser Glu Asp Pro Trp Glu Asn Lys Asp Val
        1075   1080   1085

Ile Pro Thr Ile Ile Leu Asn Lys Glu Ala Gly Thr Ser His Asp Leu
    1090   1095   1100

Val Val Asn Lys Glu Ala Gly Thr Ser His Asp Leu Val Val Leu Ser
1105   1110   1115   1120

Thr Tyr Ala Ala Ala Ile Pro Arg Arg Lys Leu Lys Ile Lys Glu Lys
            1125   1130   ⸱   1135

Leu Arg Thr Glu His His Val Phe Glu Leu Pro Asp His His Ser Ile
        1140   1145   1150

Leu Glu Gly Phe Glu Arg Arg Glu Ala Glu Asp Ile Val Pro Tyr Leu
        1155   1160   1165

Leu Ala Ile Trp Thr Pro Gly Glu Thr Val Asn Ser Ile Gln Pro Pro
    1170   1175   1180

Lys Gln Arg Cys Ala Leu Phe Glu Ser Asn Asn Thr Leu Cys Asn Glu
1185   1190   1195   1200

Asn Lys Cys Phe Gln Cys Asn Lys Thr Arg Glu Glu Glu Ser Gln Thr
            1205   1210   1215

Val Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Gly
        1220   1225   1230

Phe Pro Leu Asn Gly Thr Tyr Phe Gln Thr Asn Glu Val Phe Ala Asp
        1235   1240   1245

His Asp Ser Ser Ile Asn Pro Ile Asp Val Pro Thr Glu Leu Ile Trp
    1250   1255   1260

Asp Leu Lys Arg Arg Val Ala Tyr Leu Gly Ser Ser Val Ser Ser Ile
1265   1270   1275   1280

Cys Lys Gly Leu Ser Val Glu Ala Ile Lys Tyr Asn Phe Gln Glu Gly
            1285   1290   1295

Tyr Val Cys Val Arg Gly Phe Asp Arg Glu Asn Arg Lys Pro Lys Ser
            1300   1305   1310

Leu Val Lys Arg Leu His Cys Ser His Val Ala Ile Arg Thr Lys Glu
        1315   1320   1325

Lys Thr Glu Glu
    1330

30

<210> 12
<211> 375
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DMT3 (1DMT3) novel amino terminus

<400> 12

```
Met Glu Val Glu Gly Glu Val Arg Glu Lys Glu Ala Arg Val Lys Gly
 1               5                  10                  15

Arg Gln Pro Glu Thr Glu Val Leu His Gly Leu Pro Gln Glu Gln Ser
            20                  25                  30

Ile Phe Asn Asn Met Gln His Asn His Gln Pro Asp Ser Asp Arg Arg
            35                  40                  45

Arg Leu Ser Leu Glu Asn Leu Pro Gly Leu Tyr Asn Met Ser Cys Thr
    50                  55                  60

Gln Leu Leu Ala Leu Ala Asn Ala Thr Val Ala Thr Gly Ser Ser Ile
65                  70                  75                  80

Gly Ala Ser Ser Ser Ser Leu Ser Ser Gln His Pro Thr Asp Ser Trp
                85                  90                  95

Ile Asn Ser Trp Lys Met Asp Ser Asn Pro Trp Thr Leu Ser Lys Met
            100                 105                 110

Gln Lys Gln Gln Tyr Asp Val Ser Thr Pro Gln Lys Phe Leu Cys Asp
            115                 120                 125

Leu Asn Leu Thr Pro Glu Glu Leu Val Ser Thr Ser Thr Gln Arg Thr
            130                 135                 140

Glu Pro Glu Ser Pro Gln Ile Thr Leu Lys Thr Pro Gly Lys Ser Leu
145                 150                 155                 160

Ser Glu Thr Asp His Glu Pro His Asp Arg Ile Lys Lys Ser Val Leu
                165                 170                 175

Gly Thr Gly Ser Pro Ala Ala Val Lys Lys Arg Lys Ile Ala Arg Asn
            180                 185                 190

Asp Glu Lys Ser Gln Leu Glu Thr Pro Thr Leu Lys Arg Lys Lys Ile
            195                 200                 205

Arg Pro Lys Val Val Arg Glu Gly Lys Thr Lys Lys Ala Ser Ser Lys
    210                 215                 220

Ala Gly Ile Lys Lys Ser Ser Ile Ala Ala Thr Ala Thr Lys Thr Ser
225                 230                 235                 240

Glu Glu Ser Asn Tyr Val Arg Pro Lys Arg Leu Thr Arg Arg Ser Ile
                245                 250                 255

Arg Phe Asp Phe Asp Leu Gln Glu Glu Asp Glu Glu Phe Cys Gly Ile
            260                 265                 270
```

31

Asp Phe Thr Ser Ala Gly His Val Glu Gly Ser Ser Gly Glu Glu Asn
        275   280   285

Leu Thr Asp Thr Thr Leu Gly Met Phe Gly His Val Pro Lys Gly Arg
        290   295   300

Arg Gly Gln Arg Arg Ser Asn Gly Phe Lys Lys Thr Asp Asn Asp Cys
305   310   315   320

Leu Ser Ser Met Leu Ser Leu Val Asn Thr Gly Pro Gly Ser Phe Met
                325   330   335

Glu Ser Glu Glu Asp Arg Pro Ser Asp Ser Gln Ile Ser Leu Gly Arg
                340   345   350

Gln Arg Ser Ile Met Ala Thr Arg Pro Arg Asn Phe Arg Ser Leu Lys
        355   360   365

Lys Leu Leu Gln Arg Ile Ile
        370   375

<210> 13
<211> 8760
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> DMT3 (1DMT3) sequence from BAC T22K18

<400> 13
aatcaagtac taatgcagat ttaaggggggg tgtattgacg gcgttaaaac ggtttctcaa 60
cggaatcgta cgtagtcaca cgtgatttta ttgtttaccc cggattggtc atgcgttcct 120
tcttttccac ttgcgcggac cactcaatga cactctcttc ttttgtagca gtggcccgac 180
accagaatgc agcatttaat ctctcaaatt accattttgc tcctacctct tttacccctt 240
ttggtatttt gtgtcttttt tctttctatt tcgtgtgaaa aaggatctct tccttaatcg 300
tattatttct tccgatatct acttttattc tgttttctat ttttggtagg ttacatcttt 360
tttataaaga aaatatgagc taacacgaca ttagtgttgt taaccaaaga attggaaaaa 420
agttataaga gagataataa gattctctta cagagactca cttcagtgaa aaggaagaa 480
gcaagtggtt cccttaaggg aaaaaaaagt cacgtacgtt catatacaac tttaatacgt 540
actgtgtaac tcaatagatc gtgcagtaat attcagtcgt attagtaaga aggaatttat 600
ttgctaagta aactcaagcc tcctttttct cttttttttc ttttagtaa aaattaggct 660
agtgtttttt ttgactcagc aacactctgc ttaaatttag gagtaatttg acctattcct 720
acgagtttct aagtgaattc tgttggggtc aaagaagcaa ctagttgaat tagtggaaaa 780
tcgtttcctt tctttacgca tagttcacgt tggacactca gtctcaatgc tttcacgttt 840
cacgtagcaa caacatatat tcatcagttt gtgatcgtgc catcgtggat aagttgcaat 900
tcagtgaaac tctgcaccac tttgtgcaat tatttggccg tctaatctat ttgtgagaat 960
tttacaatct aattgttcta ttatttcatt tacttgtcat caatttatta tatttgtagc 1020
caatgaacgt tgtaattaaa gaaccaaaat aaattaatat cttgaaattt gtaacagtca 1080
ctagaagctg atttcttatt aattgtatca ctaaagtatt attaaaaacg gttacaaatt 1140
atgataatta tatatttaat aaatttcgtg tgtcacattt cttttaaact acaattatga 1200
atatctaaaa ctcattcatg catatcttaa aatttgaatt caaaactttc ttatcttatc 1260
tttaggttct taattaacag tcactaaaaa tagtcaaagt tttgaagttt atgaaaaaag 1320
ataagagtat aattaatgga tacgcctcgt aacaaattct tgtaaagtat agataatata 1380
catttgttaa atatgacacg tgtttatttt tttttaaat atgatcaaaa tatattttaa 1440
ctacctagat ggtatgtatg tctccaattt tgaataacaa gtcaattgtt attagaaatg 1500
tcataatata aagaagggaa ttaaatttgc aaagaaaaag tgaaaaacaa aggatttgta 1560
ttttggagaa aattaaggac tggatttgca aaaacgaaaa agtaacttca tgtatattgt 1620
cttccttata gtctctataa actattatct caaattttgt ctggactctg aaactcacaa 1680
gacttgactc tggcttactt ggcttcatct ttttctctct ggtaatctct cctgcaactt 1740
caagctttca ttttcaaata aatgtaatca aatctgttat tttcactcaa gaactaattg 1800

32

```
agttctctat cccttttcaat tgaaattgac attaaaatga aaagattttg aggaggtttc 1860
acctaccaca accgaatcac ttctttctcc aaatattgtt tctttcagtg gccaagaatc 1920
acaatcaatt tttgtatctt ccacaggtaa attaattgtg attgaacaga gaagaggaca 1980
agtgatcttg gttcaaaaga aatggaagtg gaaggtgaag tgagagagaa agaagctagg 2040
gttaaaggga gacaaccaga gacagaagtt ctacatggtc tgccacaaga acagtcaata 2100
tttaataaca tgcaacacaa ccatcagcct gactcagaca ggttttgtga ctcaaccgaa 2160
tttactctgt tcttctcccg gaatttccat attttctggt gattctgttt tgttaaattc 2220
tgcaaaagga agaaaataaa tcaaacattt ttcacttctt caaaacatga gtaaatgcaa 2280
aaactgagat atgtaaacac acagcaattt tttgatgaac tggttttggc tgtgtgatct 2340
ttgtgtctat gcaattacgt tttagttatt ttctactta taaggagaga tgttaactga 2400
aactgttatt gatcatacag gaggaggctt agtcttgaaa acttacctgg actatacaac 2460
atgtcttgta cacaactctt ggctctggcc aatgccacag tcgccacagg ttcatcaatt 2520
ggtgcatcat catcatcgtt aagctctcag catccaacgg attcttggat taatagctgg 2580
aagatggact ctaatccgtg gactttgagt aaaatgcaaa aacaacaatg tgagtaaaat 2640
ttgttcctga atttgtagga tcttttaaga gaaagtaagc gtttatgtgt agattaagtc 2700
agactgaaat cgattatctc ataataagtt ctcagtgatc tctcaaatca tgaatttat 2760
gtttacctga tatcaacttc ttgtcttggt gaaccacaga tgatgtgtca actccgcaga 2820
agtttctttg tgaccttaat cttacacctg aagagttggt gagcaccagt acgcaacgaa 2880
cagaacctga gtctcctcaa ataactttaa agacaccagg aaaaagtctg tctgaaactg 2940
atcatgagcc tcacgaccgt atcaagaagt ctgttcttgg aactggatct cctgcagcag 3000
taaagaaaag aaagatagca agaaatgatg agaaatctca gctggaaaca ccaacactaa 3060
agagaaaaaa gatcaggcca aaggttgtcc gtgaaggcaa aacaaaaaaa gcatcatcta 3120
aagcagggat taaaaaatcc tctattgctg ctactgctac taaaaacttct gaagagagca 3180
attatgttcg gccaaaaaga ttaacgagaa gatctatacg attcgacttt gaccttcaag 3240
aagaagatga ggaatttgt ggaatcgatt tcacatcagc aggtcacgta gagggttctt 3300
caggtgaaga aaatctaacc gatacaacac tgggaatgtt tggtcacgtc ccaaagggaa 3360
gaagagggca aagaagatcc aatggcttta aaaaaaccga caatgattgc ctcagttcta 3420
tgttgtctct tgtcaatacc ggaccaggaa gtttcatgga atcagaagaa gatcgtccga 3480
gtgattcaca aatttctctg ggaagacaga gatccattat ggcaaccaga ccgcgtaact 3540
tccgatcgtt aaagaaactt ttacaaagga ttataccaag caaacgtgat agaaaaggat 3600
gtaagcttcc tcgtggactt ccgaagctta ccgtcgcatc caagttgcaa ctaaaagtgt 3660
ttagaaagaa gcggagtcaa agaaaccgtg tagcaagcca gttcaatgca aggatattgg 3720
acttgcagtg gcgacgccaa aatccaacag gtgataaaca cacaagcaac tttcatctat 3780
aatatttttc ttagatttct atcttttgaa ttaatactag ttttacaaaa tgcaggtaca 3840
tcgctagctg atatatggga aagaagtttg actattgatg ctatcactaa gttgtttgaa 3900
gaattagaca tcaacaaaga gggtctttgc cttccacata atagagaaac tgcacttatt 3960
ctatacaaaa agtcgtatga agagcaaaag gcaatagtga agtatagcaa gaagcagaaa 4020
ccgaaagtac aattggatcc tgaaacgagt cgagtgtgga aactcttaat gtcaagtatc 4080
gactgtgacg gtgttgatgg atcagatgag gaaaaacgta aatggtggga gaggagagg 4140
aacatgttcc atggacgtgc aaactcgttc attgcgcgaa tgcgtgttgt ccaaggtatt 4200
atttattgct ttagttatga cattgttgtg tggctttata ccttagatct ttctttcttt 4260
cttttttgta tccaaagcaa catggtctta aatcaagctt atcactgcag gcaatagaac 4320
tttctcacct tggaaagggt cagtagtgga ttcagtagtg ggagttttcc taacccagaa 4380
tgtcgcagac cattcatcaa ggtatatgca ttcaagagat ttctaataag tagaagatat 4440
atgcaacaga gtggtttaga aattataact tgttcacttt tgcagttctg catatatgga 4500
tttagctgct gagtttcctg tcgagtggaa cttcaacaag ggatcatgtc atgaagagtg 4560
gggaagttca gtaactcaag aaacaatact gaatttggat ccaagaactg gagtttcaac 4620
tccaagaatt cgcaatccaa ctcgcgtcat catagaggag attgatgatg atgagaacga 4680
cattgatgct gtttgtagtc aggaatcctc taaaacaagt gacagttcca taacttctgc 4740
agaccaatca aaaacgatgc tgctggatcc atttaacaca gttttgatga acgagcaagt 4800
tgattcccaa atggtaaaag gcaaaggtca tataccatac acggatgatc ttaatgactt 4860
gtcccagggg atttcgatgg tctcatctgc ttctactcat tgtgagttga acctaaatga 4920
agtaccacct gaagtagagt tgtgcagcca tcaacaagac ccggagagta ccattcagac 4980
acaagaccag caagagagca caagaacgga ggatgtgaag aagaatagga aaaaccaac 5040
tacctccaaa ccaaagaaaa agtcaaagga atcagcaaag agcacgcaaa agaaaagcgt 5100
tgactgggat agtttgagaa aggaagcaga aagtggtggc cgaaagagag agagaacaga 5160
aagaacaatg gacacagttg attgggatgc acttcgatgt acagacgtac acaagatcgc 5220
taatataatc atcaaacgag ggatgaacaa catgcttgcc gaaagaatca aggtttgact 5280
aatcacagtg ctatatatac ctcatttata cattctaaca aggtgaattt ttttgactct 5340
ggaaattgga caggccttct taaacagact agttaaaaaa catggaagca ttgacttaga 5400
gtggctaaga gatgttcctc ctgataaagc caagtaagaa aattatttac aaatcttgag 5460
```

33

```
attatatgta gcctctggtt aaagaatata tctcagtaaa tggaatcgat agtaattgag 5520
atacatataa atgagagata cttgatagtg actactaatg gttgcaggga gtatctacta 5580
agcataaacg gattaggatt gaagagtgtg gagtgtgtta gacttttgtc actacatcag 5640
attgcattcc ctgtaagtca atgaaggata ctgaatactc agaccctaat gaatgtggaa 5700
cagatacatt aatagttacg tatttttaca aatgcaggtt gacacgaatg tcggacgcat 5760
agctgtaaga ctaggatggg ttcccttaca gccattgccc gacgagctgc aaatgcatct 5820
tttagagttg taagaaaaaa aaattaaaga tcattcttca atcatgaaag ggaacatgag 5880
aaatttacag tagttccctt taattctatt caggtaccca gttctagagt cagttcaaaa 5940
gtacctctgg ccacgcctct gcaagcttga ccaaaaaacc ttgtaagtaa attacattag 6000
catcaaccat tactctagac ccttaaactt ctctaactaa ctctaactgt atcatacaat 6060
tctaggtacg agctgcatta ccacatgata acatttggaa aggtacctca aacaaatttc 6120
aagtgtttgt ggaatgaaaa catcttaaag tggcttttcc tattttgcag gtcttttgca 6180
caaaagtaaa acccaattgc aatgcatgtc caatgaaggc ggagtgtcga cattactcta 6240
gtgcacgtgc aaggttaaac cccacaaaat tctttgttat tgccattaac atgaaaaaaa 6300
aaacactagc ttaaagagaa agagatctgc tcaaaatagt cattttaatg gttgtatgtt 6360
ctaaatgctt gtgttatatc gcagcgcacg gcttgcttta ccagaaccag aggagagtga 6420
cagaacaagt gtaatgatcc atgagaggag atctaaacgc aagcctgttg tggttaattt 6480
tcgaccatcc ttatttcttt atcaagaaaa agagcaagaa gcacaaagat cccaaaactg 6540
tgaaccaatc attgaggaac cagcatcacc agaaccagag tatatagaac atgatattga 6600
agactatcct cgggacaaaa acaacgttgg aacatcagag gatccttggg aaaataagga 6660
cgtaattcct accatcatcc tcaacaagga agctggtaca tcacatgatt tggtggtcaa 6720
caaggaagct ggtacgtcac atgatttggt ggtactaagc acatatgcag cagcaatacc 6780
tagacgtaaa ctcaagatca aggaaaagct acgcacagag caccacgtgt gagttgccac 6840
tttcaatttt ttcttctatt ataccctaaa ccgtaaaatt tgagactttc ctcagcattt 6900
atctcatact aattctcttt tacagatttg agctccctga tcaccattcc attctagaag 6960
gggttagtaa ctcttgcaaa atgatttagc aagaattttt ctacttattc ccgccttaaa 7020
aactgtttga ttatcttttt ttacagtttg agaggcgaga agctgaggat atagtccctt 7080
acttgttagc catttggacg ccaggtaaga agaaataggc acacaataaa atctgattat 7140
gatttttctt ttcaagaata ccgctatatt tttacgagtt ttcatcctta gatgtatatg 7200
actaatgtct aacaagtgat tgtaatattt ttccatacca ggtgaaaccg tgaattccat 7260
tcaaccgcca aaacaaagat gtgctttatt tgaaagcaat aatacattat gcaacgaaaa 7320
caaatgtttt caatgcaaca agacacggga agaggaatca cagactgtac gaggaactat 7380
attggtaaga ttctggtgga caattttcaa gagaatatct ctaagtagaa atataaggaa 7440
ggtataaaaa tgactaattt gtttgttaac agataccttg cagaacagca atgagaggtg 7500
gattcccttt gaatggcaca tacttccaaa ctaatgaggt aatttttccca aaaatgaatt 7560
taacttaaac aaatgatcaa aagcaacatt ctcgtcaaag ctcgatttgg actatacttg 7620
tgcaggtttt tgctgaccat gactctagca taaaccctat cgacgtccca acagaactga 7680
tatgggatct aaaaagaaga gtcgcatact taggatcctc tgtatcctcg atttgtaaag 7740
gtaaattttc aaaacaaaac tgtcgattta tgcatgtgtt tggatatata aatccaaggt 7800
cttgtctcaa tatgtttttc tcatttttt aggtttatca gtggaagcca taaaatacaa 7860
tttccaggaa ggtatgctaa tatgtcttac actgaaaaca cctttagtat caaacattga 7920
attcatgaaa agaacaaaca atagtatcaa aatcagtcac gatgtttttg ctttggcgat 7980
gtaagatgtt gataggaaag tatagaagat atagcttaag ttggttaata ctgtttttat 8040
agagctttga ggtggggttt gactagcatt gtaatatata tgcaggatat gtctgtgtaa 8100
ggggattcga cagggagaat cgtaagccaa agagtctagt gaaaagactg cattgttctc 8160
acgtagcaat cagaactaaa gagaagacag aggaatgaaa ccttccagat tgcattaaca 8220
tgttagacat atttgattca ttggtttagg gtttacatca ccaaggtcat agaggatctt 8280
agcttttcat taacttttaa attcatgcaa ctcttttag gtgtttcttt ttgttccttg 8340
ccatagtttt gggcaatgga tggatgttct ttgcaaactc aggttttttg tagtcattaa 8400
cagaaatttg cagcactaat tcatctttcc tattatctat caaagctctc agtgtttctc 8460
cataacttga tgagatttag tcactctcaa gctaattcag tctggtccta atttcaatca 8520
gatttggtaa aggaacaact gcaattgcta agtacaaatc gatccagatt tcaaacaagt 8580
tccaggttta atccaaatca tcacattcaa tcaaagacca aactagaatt caaaacatat 8640
aatctctgat tcagattcaa gaaagacaaa gcatgagaca tcattctgca agttaaccaa 8700
ttccggttat tctcgaatcc tactgaatta agcatcaatc atctaaagga acttcataag 8760
```

<210> 14
<211> 1114
<212> PRT
<213> Arabidopsis thaliana

34

<220>
<223> DMT4 (1DMT4)

<400> 14
Met Glu Phe Ser Ile Asp Arg Asp Lys Asn Leu Leu Met Val Val Pro
 1   5   10   15

Glu Thr Arg Ile Lys Thr Lys Gln Phe Glu Lys Val Tyr Val Arg Arg
                20   25   30

Lys Ser Ile Lys Leu Pro Gln Asn Ser Met Val His Asn Thr Leu Ile
            35   40   45

Lys Met Ala Arg Gln Arg Ile Gln Lys Ser Met Lys Glu Ser Val Met
        50   55   60

Asn Gln His Ile Phe Lys Asn Phe Asp Ser Tyr Leu Ser Val Ile Tyr
 65   70   75   80

His Pro Cys Cys Phe Val Ile Asn Asn Ser Gln Thr Thr His Lys Lys
            85   90   95

Lys Glu Lys Lys Asn Ser Lys Glu Lys His Gly Ile Lys His Ser Glu
            100   105   110

Ser Glu His Leu Gln Asp Asp Ile Ser Gln Arg Val Thr Gly Lys Gly
            115   120   125

Arg Arg Arg Asn Ser Lys Gly Thr Pro Lys Lys Leu Arg Phe Asn Arg
            130   135   140

Pro Arg Ile Leu Glu Asp Gly Lys Lys Pro Arg Asn Pro Ala Thr Thr
145   150   155   160

Arg Leu Arg Thr Ile Ser Asn Lys Arg Arg Lys Lys Asp Ile Asp Ser
                165   170   175

Glu Asp Glu Val Ile Pro Glu Leu Ala Thr Pro Thr Lys Glu Ser Phe
            180   185   190

Pro Lys Arg Arg Lys Asn Glu Lys Ile Lys Arg Ser Val Ala Arg Thr
            195   200   205

Leu Asn Phe Lys Gln Glu Ile Val Leu Ser Cys Leu Glu Phe Asp Lys
    210   215   220

Ile Cys Gly Pro Ile Phe Pro Arg Gly Lys Lys Arg Thr Thr Thr Arg
225   230   235   240

Arg Arg Tyr Asp Phe Leu Cys Phe Leu Leu Pro Met Pro Val Trp Lys
            245   250   255

Lys Gln Ser Arg Arg Ser Lys Arg Arg Lys Asn Met Val Arg Trp Ala
            260   265   270

Arg Ile Ala Ser Ser Ser Lys Leu Leu Glu Glu Thr Leu Pro Leu Ile
            275   280   285

Val Ser His Pro Thr Ile Asn Gly Gln Ala Asp Ala Ser Leu His Ile
    290   295   300

Asp Asp Thr Leu Val Arg His Val Val Ser Lys Gln Thr Lys Lys Ser
305   310   315   320

Ala Asn Asn Val Ile Glu His Leu Asn Arg Gln Ile Thr Tyr Gln Lys
            325   330   335

Asp His Gly Leu Ser Ser Leu Ala Asp Val Pro Leu His Ile Glu Asp
        340   345   350

Thr Leu Ile Lys Ser Ala Ser Ser Val Leu Ser Glu Arg Pro Ile Lys
        355   360   365

Lys Thr Lys Asp Ile Ala Lys Leu Ile Lys Asp Met Gly Arg Leu Lys
    370   375   380

Ile Asn Lys Lys Val Thr Thr Met Ile Lys Ala Asp Lys Lys Leu Val
385   390   395   400

Thr Ala Lys Val Asn Leu Asp Pro Glu Thr Ile Lys Glu Trp Asp Val
            405   410   415

Leu Met Val Asn Asp Ser Pro Ser Arg Ser Tyr Asp Asp Lys Glu Thr
        420   425   430

Glu Ala Lys Trp Lys Lys Glu Arg Glu Ile Phe Gln Thr Arg Ile Asp
    435   440   445

Leu Phe Ile Asn Arg Met His Arg Leu Gln Gly Asn Arg Lys Phe Lys
    450   455   460

Gln Trp Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr
465   470   475   480

Gln Asn Thr Thr Asp Tyr Leu Ser Ser Asn Ala Phe Met Ser Val Ala
            485   490   495

Ala Lys Phe Pro Val Asp Ala Arg Glu Gly Leu Ser Tyr Tyr Ile Glu
        500   505   510

Glu Pro Gln Asp Ala Lys Ser Ser Glu Cys Ile Ile Leu Ser Asp Glu
    515   520   525

Ser Ile Ser Lys Val Glu Asp His Glu Asn Thr Ala Lys Arg Lys Asn
    530   535   540

Glu Lys Thr Gly Ile Ile Glu Asp Glu Ile Val Asp Trp Asn Asn Leu
545   550   555   560

Arg Arg Met Tyr Thr Lys Glu Gly Ser Arg Pro Glu Met His Met Asp
            565   570   575

Ser Val Asn Trp Ser Asp Val Arg Leu Ser Gly Gln Asn Val Leu Glu
            580   585   590

Thr Thr Ile Lys Lys Arg Gly Gln Phe Arg Ile Leu Ser Glu Arg Ile
        595   600   605

Leu Lys Phe Leu Asn Asp Glu Val Asn Gln Asn Gly Asn Ile Asp Leu
    610   615   620

36

```
Glu Trp Leu Arg Asn Ala Pro Ser His Leu Val Lys Arg Tyr Leu Leu
625             630             635             640

Glu Ile Glu Gly Ile Gly Leu Lys Ser Ala Glu Cys Val Arg Leu Leu
            645             650             655

Gly Leu Lys His His Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile
        660             665             670

Ala Val Arg Leu Gly Leu Val Pro Leu Glu Pro Leu Pro Asn Gly Val
        675             680             685

Gln Met His Gln Leu Phe Glu Tyr Pro Ser Met Asp Ser Ile Gln Lys
    690             695             700

Tyr Leu Trp Pro Arg Leu Cys Lys Leu Pro Gln Glu Thr Leu Tyr Glu
705             710             715             720

Leu His Tyr Gln Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Thr
            725             730             735

Ile Pro Asn Cys Asn Ala Cys Pro Met Lys Ser Glu Cys Lys Tyr Phe
            740             745             750

Ala Ser Ala Tyr Val Ser Ser Lys Val Leu Leu Glu Ser Pro Glu Glu
        755             760             765

Lys Met His Glu Pro Asn Thr Phe Met Asn Ala His Ser Gln Asp Val
    770             775             780

Ala Val Asp Met Thr Ser Asn Ile Asn Leu Val Glu Glu Cys Val Ser
785             790             795             800

Ser Gly Cys Ser Asp Gln Ala Ile Cys Tyr Lys Pro Leu Val Glu Phe
            805             810             815

Pro Ser Ser Pro Arg Ala Glu Ile Pro Glu Ser Thr Asp Ile Glu Asp
            820             825             830

Val Pro Phe Met Asn Leu Tyr Gln Ser Tyr Ala Ser Val Pro Lys Ile
        835             840             845

Asp Phe Asp Leu Asp Ala Leu Lys Lys Ser Val Glu Asp Ala Leu Val
    850             855             860

Ile Ser Gly Arg Met Ser Ser Ser Asp Glu Glu Ile Ser Lys Ala Leu
865             870             875             880

Val Ile Pro Thr Pro Glu Asn Ala Cys Ile Pro Ile Lys Pro Pro Arg
            885             890             895

Lys Met Lys Tyr Tyr Asn Arg Leu Arg Thr Glu His Val Val Tyr Val
        900             905             910

Leu Pro Asp Asn His Glu Leu Leu His Asp Phe Glu Arg Arg Lys Leu
    915             920             925

Asp Asp Pro Ser Pro Tyr Leu Leu Ala Ile Trp Gln Pro Gly Glu Thr
    930             935             940
```

37

Ser Ser Ser Phe Val Pro Pro Lys Lys Lys Cys Ser Ser Asp Gly Ser
945   950   955   960

Lys Leu Cys Lys Ile Lys Asn Cys Ser Tyr Cys Trp Thr Ile Arg Glu
                965   970   975

Gln Asn Ser Asn Ile Phe Arg Gly Thr Ile Leu Val Phe Ala Asp His
            980   985   990

Glu Thr Ser Leu Asn Pro Ile Val Phe Arg Arg Glu Leu Cys Lys Gly
        995   1000   1005

Leu Glu Lys Arg Ala Leu Tyr Cys Gly Ser Thr Val Thr Ser Ile Phe
    1010   1015   1020

Lys Leu Leu Asp Thr Arg Arg Ile Glu Leu Cys Phe Trp Thr Gly Phe
1025   1030   1035   1040

Leu Cys Leu Arg Ala Phe Asp Arg Lys Gln Arg Asp Pro Lys Glu Leu
            1045   1050   1055

Val Arg Arg Leu His Thr Pro Pro Asp Glu Arg Gly Pro Asn Gly Phe
            1060   1065   1070

His Ile Val Val Val Asp Glu Lys Glu Glu Ser Pro Arg Val Gly Leu
        1075   1080   1085

Met Val Met Pro Gly Phe Trp Ile Gly Gly Ser Val Ile Gln Asn Arg
    1090   1095   1100

Val Tyr Val Ser Gly Val Lys Val Leu Glu
1105   1110

<210> 15
<211> 372
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> DMT4 (1DMT4) novel amino terminus

<400> 15
Met Glu Phe Ser Ile Asp Arg Asp Lys Asn Leu Leu Met Val Val Pro
    1   5   10   15

Glu Thr Arg Ile Lys Thr Lys Gln Phe Glu Lys Val Tyr Val Arg Arg
            20   25   30

Lys Ser Ile Lys Leu Pro Gln Asn Ser Met Val His Asn Thr Leu Ile
        35   40   45

Lys Met Ala Arg Gln Arg Ile Gln Lys Ser Met Lys Glu Ser Val Met
    50   55   60

Asn Gln His Ile Phe Lys Asn Phe Asp Ser Tyr Leu Ser Val Ile Tyr
65   70   75   80

His Pro Cys Cys Phe Val Ile Asn Asn Ser Gln Thr Thr His Lys Lys
            85   90   95

38

```
Lys Glu Lys Lys Asn Ser Lys Glu Lys His Gly Ile Lys His Ser Glu
            100                 105                 110

Ser Glu His Leu Gln Asp Asp Ile Ser Gln Arg Val Thr Gly Lys Gly
            115                 120                 125

Arg Arg Arg Asn Ser Lys Gly Thr Pro Lys Lys Leu Arg Phe Asn Arg
    130                 135                 140

Pro Arg Ile Leu Glu Asp Gly Lys Lys Pro Arg Asn Pro Ala Thr Thr
145                 150                 155                 160

Arg Leu Arg Thr Ile Ser Asn Lys Arg Arg Lys Lys Asp Ile Asp Ser
                165                 170                 175

Glu Asp Glu Val Ile Pro Glu Leu Ala Thr Pro Thr Lys Glu Ser Phe
            180                 185                 190

Pro Lys Arg Arg Lys Asn Glu Lys Ile Lys Arg Ser Val Ala Arg Thr
            195                 200                 205

Leu Asn Phe Lys Gln Glu Ile Val Leu Ser Cys Leu Glu Phe Asp Lys
    210                 215                 220

Ile Cys Gly Pro Ile Phe Pro Arg Gly Lys Lys Arg Thr Thr Thr Arg
225                 230                 235                 240

Arg Arg Tyr Asp Phe Leu Cys Phe Leu Leu Pro Met Pro Val Trp Lys
            245                 250                 255

Lys Gln Ser Arg Arg Ser Lys Arg Arg Lys Asn Met Val Arg Trp Ala
            260                 265                 270

Arg Ile Ala Ser Ser Ser Lys Leu Leu Glu Glu Thr Leu Pro Leu Ile
            275                 280                 285

Val Ser His Pro Thr Ile Asn Gly Gln Ala Asp Ala Ser Leu His Ile
    290                 295                 300

Asp Asp Thr Leu Val Arg His Val Val Ser Lys Gln Thr Lys Lys Ser
305                 310                 315                 320

Ala Asn Asn Val Ile Glu His Leu Asn Arg Gln Ile Thr Tyr Gln Lys
                325                 330                 335

Asp His Gly Leu Ser Ser Leu Ala Asp Val Pro Leu His Ile Glu Asp
            340                 345                 350

Thr Leu Ile Lys Ser Ala Ser Ser Val Leu Ser Glu Arg Pro Ile Lys
            355                 360                 365

Lys Thr Lys Asp
    370
```

<400> 16
```
gctatggatg tcaacagaga gaattacgaa ttgggtttac cgatcattga gaaagccggc 60
gttgctcaca agatcgactt cagggaaggc cctgctcttc ccgttcttga tgaaatcgtt 120
gctgacgtaa gcattcttct ttctgacgta attaacaaaa aagatgatga agataatgaa 180
ataattaaaa actcatggcc taattaggtt gatttaatat cttgatgaga atttctgtat 240
acgcaaattt gtttcctttt tcatagaaga aagtgtggta actgattatt gtgtgtggtt 300
gggtgcagga gaagaaccat ggaacatatg actttatatt cgttgatgct gacaaagaca 360
actacatcaa ctaccacaag cgtttgatcg atcttgtgaa aattggagga gtgattggct 420
acgacaacac tctgtggaat ggttctgtcg tggctcctcc tgatgcacca atgaggaagt 480
acgttcgtta ctacagagac tttgttcttg agcttaacaa ggctcttgct gctgaccctc 540
ggatcgagat ctgtatgctc cctgttggtg atggaatcac tatctgccgt cggatcagtt 600
gatttgactc ctccctactc tgagtttgtc cacagtggat tactttccat cttcttatac 660
ctttcaatcg cattttcacc aaccactaaa atggaccttt ttatgtattt gtgttaagta 720
atatctccat tgtccttgtt ttgctttctt ctgaacaaag aaataatatg taccttactt 780
ttcttcttgg tctcgttctt ttgtttttct ccatgataca acatctaaag aaattatttg 840
tgtcacagca acgtaagtcg ataaaattag ttgaacatat tgagaaaaag ttatcataga 900
ccttcaattg ttgaaagtcg atgttggtat ttgtcaattg atattagatt accaaataaa 960
tattagacag taagaaacga acaaagtagg aagatgtagg tcaccggtct ttgaaaattt 1020
atcagataga attcataata cacagttagg tagtttcagt tgagagttaa aagggaaaaa 1080
tatgtaattg tgtgtgataa atacgtcaaa aattagttga tgagcaaaat cgtaaacaaa 1140
aatacttttt tgcattagtt ttgttggatt ccctataaat acgggttccc atatctaact 1200
cgtagttagc ataattataa gcaacaaata aacacaaaat actgaattta gaaattttcc 1260
agaaaattaa ttagagattt tacattattt ttacaaactt tagtgaatta tttcttaaac 1320
gtatgttagt tatttattaa ctgaagtttc acatatttga tagaataaca tttaaataaa 1380
aaaatttgaa gtaaggttag aatgttctta taatacttta taactttttt aaaaggtaca 1440
agccaaaatt atcgcaaatg taaataataa atcattgtaa aaatcttaaa ctaattaaaa 1500
gatctaacgc aatctaaaca aagatttggt atcatcgccc atttatgttt tgatataatc 1560
aaaactggtt aataattaaa ttaaattatc aatttcttaa ttagttagaa ttcttgttaa 1620
tgtaatcaac tcaccattat tttaattatt taaaatatgg gttaatatct cttaatcata 1680
tctaagatga tattttcttc catttatgaa aagaaaaata tgttaattaa gcattaaaaa 1740
gaaggaaaaa ataatttaaa taatattaaa tatatataca tcgtttttag agttcgagtt 1800
cttccgtatt tacagtttct ctttttttcca aagcagggtt tggattggta gtttttctgg 1860
attaattttg tctcaaattc tttcttcttt ttatttttttt ttgtgaaatt ctttgtttta 1920
attggtgtga catcgtttcc aaaatatttt caaatttgat tgcttttgaa gttttttttt 1980
ttttctatg ttttggaatt cattatacta gcgttgttgt ttttctttct gcaagagtaa 2040
tggagttttc aatagatcga gacaaaaatc ttctcatggt tgttccagag acacgtatca 2100
aaacaaaaca atttgaaaaa gtttatgtga gaagaaaatc tattaagctt ccacaaaatt 2160
cggtaatttt tccacatgaa atcaaagatc gtggtgaaga agagagtaag gagaaggaat 2220
ttttccatca aggtaaacaa aatctctaat accttaatta cttccgttta gtaattctcc 2280
ttttacttgt tttttttttta atgagagtat gtgacaattt cataaagaaa ttagttgttt 2340
gacatacgag atggtttttt gactaattat atttttttgtt ttgaaagatt tccaagctaa 2400
ttttaatgag catatttttg attttattga ttgaggaaat tttcagaatt tcgacattta 2460
agtttttttt ttgttttaaa tatacttttg attcgatgat aagagattgg gaaagcagac 2520
taatgatgtt ttgttgtcac gttcattgat tagagatctc ttatattcat atttgtctac 2580
aatatatcat gcatgtgttg atttgtttcg ttaattcaat ttttttttttt tcatgttgac 2640
agatggttca caacacactt atcaaaatgg cgagacaaag aattcaaaag agcatgaaag 2700
aaagtgtgat gaatcagcac atcttcaagg taaataattt taaattcatt cttaaaaaag 2760
ttagcttatt ggtaagttca ttacaattta tatttaacca tcgtcacttt ttatttaacg 2820
agtttgataa gcattttcaa aacctgtcct tcatctgccg atgcagatgt ggttatgttc 2880
atctttgatt ttattgattg aggattttt cagaatttcg attcatactt gtctgtaata 2940
tatcatccat gttgtttttgt aatcagttaa ttcacttatt ttattttttaa ctttttattgt 3000
aacagataat tcacaaacca cccataaaaa aaaggagaag aagaattcaa aagaaaagca 3060
tggaataaag cattctgaat cagaacatct tcaaggtaaa tacttttgaa ttcattcatt 3120
aaaaaaacag tttatttgta agttcattac agtttatata tatttaaatt gtttatgata 3180
atgtattttt gcacaatcga ctaatcatta cccactcatt catttatatt ttattttatg 3240
gtgaaagatg atatttcgca acgtgttacc ggaaaaggaa ggagaaggaa ttcaaaaggg 3300
acaccaaaaa aactgaggtt taataggcct cggatcttgg aagacggaaa gaaaccaaga 3360
aatcccgcca ccactcgact gagaactata tccaacaaga ggaggaaaaa ggacatagac 3420
agtgaagatg aagttatacc agagcttgca actccaacaa aggaaagctt tccaaagaga 3480
agaaagaacg agaagattaa gagatccgtg gctcggactt taaattttaa gcaagaaatt 3540
gttctgagtt gtcttgagtt cgacaagatt tgtggaccaa tttttccaag agggaaaaag 3600
```

```
aggaccacca cacgacgcag atatgatttc ctttgttttt tacttccgat gcctgtttgg 3660
aaaaaacaat caagaaggtc taagcgtagg aaaaatatgg tcagatgggc tagaattgct 3720
tcttcttcaa aactgctaga agaaactttg cctttaatag taagtcatcc gactattaat 3780
ggacaagcag atgcttcttt acacattgat ggtaatcgag ttttttttt gttaatttat 3840
ctgttacatc aaaattgttt atgcttatat ctaaagtatc attgtgtatt atttttgca 3900
gacacactcg tgagacatgt agtctcaaag caaaccaaga aaagtgctaa caatgtcatt 3960
gagcatttaa atcgacaaat aacttatcag aaagatcacg gtctctcatc tctggcagat 4020
gttcctttgc acattgaagg taatctagtc ttatttttgt tcttttttaa tatattgatt 4080
aaaaagattg tgatatattt atttaatata tttttgttat attatatcta tattttattg 4140
tttgtacttt ttttttgtag atacactaat aaaatcggct agttctgtac tttcagaacg 4200
acccatcaag aaaactaagg atattgctaa gttaatcaaa gatatgggaa gattaaagat 4260
caataaaaag gtaacaacga tgatcaaagc tgacaagaaa ctcgttacgg caaaggttaa 4320
tcttgatcca gagaccatta aagagtggga tgtcttaatg gtgaatgatt caccaagccg 4380
atcatatgac gataaggaga cggaggccaa atggaaaaaa gaaagagaga tttttcaaac 4440
ccggatagat cttttcatta accggatgca tcgcttacaa ggtacattat tgttattatc 4500
attattgtta ttatgatcta tttatacttg tattctaaat tagcttacac atatatataa 4560
ggaatccaag tataagtgag tatgctaagt atatgatcat tttttgaaat tatgtttcct 4620
tccatgatgt ttaaatgatt gtcttgcagg caatagaaag tttaaacagt ggaaaggctc 4680
agttgttgac tcagtggttg gagttttttt gacacaaaat actaccgact atctttcaag 4740
gtaaaatctt tgtttaaatt gttaagaaat ttgaaaaact aattcatata atagatgatc 4800
actttgattg tgagtttcta cagcaacgcg tttatgagcg tggctgcaaa atttcctgtt 4860
gatgcaagag aaggtctatc atactatatt gaggaacctc aagatgctaa aagttctgaa 4920
tgtatcattt tatctgatga gtcaatatca aaggtggaag atcatgagaa tactgcaaaa 4980
aggaaaaacg agaaaaccgg tattatagaa gatgagatag ttgactggaa caatcttaga 5040
aggatgtaca cgaaagaagg atctcgtccc gaaatgcata tggactctgt taattggagt 5100
gacgtgagat tatctggcca aaatgttttg gaaaccacca ttaaaaaacg tggacaattc 5160
aggattcttt cagaaagaat attggtaaga aaaacaaaac ttctaatgaa ctttgtgaat 5220
aatttattca aatgatttaa gactaacact tttttttttt tccttgtttt ctcaagaaat 5280
ttcttaacga tgaagttaac caaaatggaa atattgatct ggaatggctt cgaaatgctc 5340
catcacattt agtgaagtat gtttatgttg gtttttatgt tctcatagat ctcattatta 5400
gtaagcgatc ataaactctt tctattattt tatcaggaga tatctgttgg aaatcgaagg 5460
gatagggctg aaaagtgctg agtgcgtacg actgttagga cttaaacatc atgcgtttcc 5520
ggtatgaaaa tattattatg atttttcatt taacatatat tattaatttt tactgataaa 5580
acccatgtgt taatgtgtag gttgacacaa atgttggtcg tatagcagtt cgactaggtc 5640
tggttcctct tgaacctta ccaaatggag ttcaaatgca tcaactattc gagttatgtt 5700
ttctcattaa tttgattaag aaaatacatt acaagttact aacaactatc tcctatcgat 5760
aaacatgaac tcgtttcagg tacccttcaa tggattcgat tcaaaagtac ctttggccac 5820
gattgtgtaa acttccccaa gaaactttgt aagttcaaat gttttttcctc aatttaagaa 5880
gccaactatt tttacgccat ttgaacacat attacctaat tttatttcta aatatttta 5940
cagatatgaa ctacattatc aaatgataac atttggaaag gtgtgcgtta ctttttttctt 6000
ttttatatta atgaataaaa taatattgtt ggtttaatca aattttgtca actttaggtt 6060
ttctgcacaa aaactattcc taattgtaat gcatgtccaa tgaagtcaga atgcaaatat 6120
tttgcaagtg catatgtcag gtacaatctt ttttctcttt cctactttga tacttagata 6180
taacttaatt tgttaattcc ataaatatta aagaaaaatc ttagaataat cataaaaaat 6240
aattgctaaa cgtctcagct attttatata ataaattttc taaatattga gagtgaattt 6300
gagttttaat aattacatta tatatataaa tatataatgt tagaattgac aaattgtgtt 6360
ttttttttaat agttctaaag ttcttctcga gagtccagaa gaaaagatgc atgagcctaa 6420
tacttttatg aatgcacatt ctcaagacgt tgctgtagat atgacatcaa atataaattt 6480
ggtagaagaa tgtgtttctt ctggatgtag cgatcaagct atatgttata agccactagt 6540
tgagtttcct tcgtccccaa gagcggaaat tcccgagtca acagacattg aagatgttcc 6600
attcatgaat ctttatcagt catatgctag tgttcctaaa attgattttg acttggatgc 6660
attgaagaaa agtgtagaag atgcacttgt aataagtggc aggatgagca gttctgatga 6720
agaaatatca aaagcattag tgattcccac tcctgaaaat gcatgcattc ctatcaaacc 6780
acctcggaaa atgaagtatt ataatcgact aagaactgaa catgtggtgt aagtatcttt 6840
atgtaaatac tgattatacc atataattta tatgcatttt ttgggaatat ataatctaat 6900
acttgttttt tttgcagtta tgtgcttcct gataatcatg agctgctaca cgatgtaagt 6960
atacacatac tttaagctac aaaaaaatgc aactcttttg tataattaat tagaaaatgc 7020
ttttggtttt ttacatatat tatatagttt gagagaagaa aacttgatga tccaagtcct 7080
taccttcttg cgatttggca accaggtata atacaagcat aatttatcat tgttcacata 7140
actataaact aaattttttca ttcgaataat ttttaggtga aacatcatcc tcgttcgttc 7200
caccaaagaa aaagtgtagt tctgatggat caaagctttg caagataaag aattgttcat 7260
```

41

```
attgttggac tatacgagaa caaaactcca acatttttcg cggaacaatt ttggtaaaca 7320
aaatttacaa tttgatattt taacattggt gacttgaaac tcacataaat tcaattgatc 7380
agattccatg tagaacagca atgcgagggg cctttccact taatggaaca tacttccaaa 7440
ccaatgaggc aagcattttt tcttataatt ttttgtctga gtttttactt aatggtttta 7500
aagagaacac aatggtttat ttttccaggt ttttgctgat catgagacaa gcttaaaccc 7560
cattgtcttt cgtagggagt tgtgtaaggg actagaaaaa cgtgcactat attgtggttc 7620
aacagtgaca tctattttta aacttttaga cacaagacgg attgaacttt gcttttggac 7680
aggtaacaaa cataaatata tattaaattt tttgttgaat tatgaagtta aaataactgt 7740
ggaatgttgt gtggtgctgt gcagggtttt tatgtttgag agcatttgat cgaaagcaac 7800
gagatccaaa agagcttgtc cgacgtctac acactccacc tgatgagaga gggccaaagt 7860
ttatgagtga tgatgatata tagtttcatt ttattctttt tggtctagtt agcaaattat 7920
ttaaacgaac gaatcttttc ttataataac aagcgattca acgattgagt aaatgcacgt 7980
acgtattgtt tcttgattta aatgcatgta cattataatt atttcacaag tggttttcat 8040
atagtagttg tggatgaaaa agaagagagc ccaagagttg gtcttatggt tatgcctggg 8100
ttttggattg gtggcagtgt cattcaaaac cgagtttatg tttctggtgt gaaggtcctt 8160
gagtgaagga tttcaggaac tgtcttaatg cttcttccca ctttgttgtg caactttttat 8220
tttctctttg ttataagcaa gcctatatgt atcaatgata cagtatcatc tattgttcaa 8280
aaaaattgga attaatatct tcttcgtctc aacatctttg ggtcgatcgt tattcgatga 8340
cagtagcaac tagcgagtct cttgtgatat atcctagcca agcgacctca aaactttttt 8400
tacttcgatt gttgtcagta tttctgtttc agacgttttt agcaaaaaag ttctcatggt 8460
gataaaatta ggcttaaaac agtatgactc tgtctttaag actcagtttc agatagtaat 8520
aataaaatta cataaacaaa gagtggtcat agacgtgtat ctgtaagtgt tgtcagagat 8580
```


<210> 17
<211> 1952
<212> PRT
<213> Oryza sativa

<220>
<223> rice DMT1, DMTRICE (1DMTRICE)

<400> 17
Met Gln Asp Phe Gly Gln Trp Leu Pro Gln Ser Gln Thr Thr Ala Asp
 1   5   10   15

Leu Tyr Phe Ser Ser Ile Pro Ile Pro Ser Gln Phe Asp Thr Ser Ile
            20   25   30

Glu Thr Gln Thr Arg Thr Ser Ala Val Val Ser Ser Glu Lys Glu Ser
        35   40   45

Ala Asn Ser Phe Val Pro His Asn Gly Thr Gly Leu Val Glu Arg Ile
    50   55   60

Ser Asn Asp Ala Gly Leu Thr Glu Val Val Gly Ser Ser Ala Gly Pro
65   70   75   80

Thr Glu Cys Ile Asp Leu Asn Lys Thr Pro Ala Arg Lys Pro Lys Lys
                85   90   95

Lys Lys His Arg Pro Lys Val Leu Lys Asp Asp Lys Pro Ser Lys Thr
            100   105   110

Pro Lys Ser Ala Thr Pro Ile Pro Ser Thr Glu Lys Val Glu Lys Pro
        115   120   125

Ser Gly Lys Arg Lys Tyr Val Arg Lys Lys Thr Ser Pro Gly Gln Pro
    130   135   140

42

```
Pro Ala Glu Gln Ala Ala Ser Ser His Cys Arg Ser Glu Leu Lys Ser
145             150             155             160

Val Lys Arg Ser Leu Asp Phe Gly Gly Glu Val Leu Gln Glu Ser Thr
            165             170             175

Gln Ser Gly Ser Gln Val Pro Val Ala Glu Ile Cys Thr Gly Pro Lys
            180             185             190

Arg Gln Ser Ile Pro Ser Thr Ile Gln Arg Asp Ser Gln Ser Gln Leu
        195             200             205

Ala Cys His Val Val Ser Ser Thr Ser Ser Ile His Thr Ser Ala Ser
    210             215             220

Gln Met Val Asn Ala His Leu Phe Pro Pro Asp Asn Met Pro Asn Gly
225             230             235             240

Val Leu Leu Asp Leu Asn Asn Ser Thr Ser Gln Leu Gln Asn Glu His
            245             250             255

Ala Lys Phe Val Asp Ser Pro Ala Arg Leu Phe Gly Ser Arg Ile Arg
            260             265             270

Gln Thr Ser Gly Lys Asn Ser Leu Leu Glu Ile Tyr Ala Gly Met Ser
        275             280             285

Asp Arg Asn Val Pro Asp Leu Asn Ser Ser Ile Ser Gln Thr His Ser
    290             295             300

Met Ser Thr Asp Phe Ala Gln Tyr Leu Leu Ser Ser Ser Gln Ala Ser
305             310             315             320

Val Arg Glu Thr Gln Met Ala Asn Gln Met Leu Asn Gly His Arg Met
            325             330             335

Pro Glu Asn Pro Ile Thr Pro Ser His Cys Ile Glu Arg Ala Ala Leu
            340             345             350

Lys Glu His Leu Asn His Val Pro His Ala Lys Ala Ala Val Met Asn
        355             360             365

Gly Gln Met Pro His Ser Tyr Arg Leu Ala Gln Asn Pro Ile Leu Pro
    370             375             380

Pro Asn His Ile Glu Gly Tyr Gln Val Met Glu Asn Leu Ser Glu Leu
385             390             395             400

Val Thr Thr Asn Asp Tyr Leu Thr Ala Ser Pro Phe Ser Gln Thr Gly
            405             410             415

Ala Ala Asn Arg Gln His Asn Ile Gly Asp Ser Met His Ile His Ala
            420             425             430

Leu Asp Pro Arg Arg Glu Ser Asn Ala Ser Ser Gly Ser Trp Ile Ser
        435             440             445

Leu Gly Val Asn Phe Asn Gln Gln Asn Asn Gly Trp Ala Ser Ala Gly
    450             455             460
```

43

Ala Ala Asp Ala Ala Ser Ser His Ala Pro Tyr Phe Ser Glu Pro His
465   470   475   480

Lys Arg Met Arg Thr Ala Tyr Leu Asn Asn Tyr Pro Asn Gly Val Val
            485   490   495

Gly His Phe Ser Thr Ser Ser Thr Asp Leu Ser Asn Asn Glu Asn Glu
            500   505   510

Asn Val Ala Ser Ala Ile Asn Ser Asn Val Phe Thr Leu Ala Asp Ala
        515   520   525

Gln Arg Leu Ile Ala Arg Glu Lys Ser Arg Ala Ser Gln Arg Met Ile
    530   535   540

Ser Phe Arg Ser Ser Lys Asn Asp Met Val Asn Arg Ser Glu Met Val
545   550   555   560

His Gln His Gly Arg Pro Ala Pro His Gly Ser Ala Cys Arg Glu Ser
            565   570   575

Ile Glu Val Pro Asp Lys Gln Phe Gly Leu Met Thr Glu Glu Leu Thr
            580   585   590

Gln Leu Pro Ser Met Pro Asn Asn Pro Gln Arg Glu Lys Tyr Ile Pro
        595   600   605

Gln Thr Gly Ser Cys Gln Leu Gln Ser Leu Glu His Asp Met Val Lys
    610   615   620

Gly His Asn Leu Ala Gly Glu Leu His Lys Gln Val Thr Ser Pro Gln
625   630   635   640

Val Val Ile Gln Ser Asn Phe Cys Val Thr Pro Pro Asp Val Leu Gly
            645   650   655

Arg Arg Thr Ser Gly Glu His Leu Arg Thr Leu Ile Ala Pro Thr His
        660   665   670

Ala Ser Thr Cys Lys Asp Thr Leu Lys Ala Leu Ser Cys Gln Leu Glu
    675   680   685

Ser Ser Arg Asp Ile Ile Arg Pro Pro Val Asn Pro Ile Gly Pro Ser
    690   695   700

Ser Ala Asp Val Pro Arg Thr Asp Asn His Gln Val Lys Val Ser Glu
705   710   715   720

Glu Thr Val Thr Ala Lys Leu Pro Glu Lys Arg Lys Val Gly Arg Pro
            725   730   735

Arg Lys Glu Leu Lys Pro Gly Glu Lys Pro Lys Pro Arg Gly Arg Pro
            740   745   750

Arg Lys Gly Lys Val Val Gly Gly Glu Leu Ala Ser Lys Asp Ser His
        755   760   765

Thr Asn Pro Leu Gln Asn Glu Ser Thr Ser Cys Ser Tyr Gly Pro Tyr
    770   775   780

44

Ala Gly Glu Ala Ser Val Gly Arg Ala Val Lys Ala Asn Arg Val Gly
785   790   795   800

Glu Asn Ile Ser Gly Ala Met Val Ser Leu Leu Asp Ser Leu Asp Ile
                805   810   815

Val Ile Gln Lys Ile Lys Val Leu Asp Ile Asn Lys Ser Glu Asp Pro
            820   825   830

Val Thr Ala Glu Pro His Gly Ala Leu Val Pro Tyr Asn Gly Glu Phe
            835   840   845

Gly Pro Ile Val Pro Phe Glu Gly Lys Val Lys Arg Lys Arg Ser Arg
        850   855   860

Ala Lys Val Asp Leu Asp Pro Val Thr Ala Leu Met Trp Lys Leu Leu
865   870   875   880

Met Gly Pro Asp Met Ser Asp Cys Ala Glu Gly Met Asp Lys Asp Lys
                885   890   895

Glu Lys Trp Leu Asn Glu Glu Arg Lys Ile Phe Gln Gly Arg Val Asp
            900   905   910

Ser Phe Ile Ala Arg Met His Leu Val Gln Gly Asp Arg Arg Phe Ser
        915   920   925

Pro Trp Lys Gly Ser Val Val Asp Ser Val Val Gly Val Phe Leu Thr
    930   935   940

Gln Asn Val Ser Asp His Leu Ser Ser Ser Ala Phe Met Ala Leu Ala
945   950   955   960

Ala Lys Phe Pro Val Lys Pro Glu Ala Ser Glu Lys Pro Ala Asn Val
                965   970   975

Met Phe His Thr Ile Ser Glu Asn Gly Asp Cys Ser Gly Leu Phe Gly
            980   985   990

Asn Ser Val Lys Leu Gln Gly Glu Ile Leu Val Gln Glu Ala Ser Asn
        995   1000   1005

Thr Ala Ala Ser Phe Ile Thr Thr Glu Asp Lys Glu Gly Ser Asn Ser
    1010   1015   1020

Val Glu Leu Leu Gly Ser Ser Phe Gly Asp Gly Val Asp Gly Ala Ala
1025   1030   1035   1040

Gly Val Tyr Ser Asn Ile Tyr Glu Asn Leu Pro Ala Arg Leu His Ala
            1045   1050   1055

Thr Arg Arg Pro Val Val Gln Thr Gly Asn Ala Val Glu Ala Glu Asp
        1060   1065   1070

Gly Ser Leu Glu Gly Val Val Ser Ser Glu Asn Ser Thr Ile Ser Ser
    1075   1080   1085

Gln Asn Ser Ser Asp Tyr Leu Phe His Met Ser Asp His Met Phe Ser
    1090   1095   1100

45

Ser Met Leu Leu Asn Phe Thr Ala Glu Asp Ile Gly Ser Arg Asn Met
1105   1110   1115   1120

Pro Lys Ala Thr Arg Thr Thr Tyr Thr Glu Leu Leu Arg Met Gln Glu
              1125   1130   1135

Leu Lys Asn Lys Ser Asn Glu Thr Ile Glu Ser Ser Glu Tyr His Gly
         1140   1145   1150

Val Pro Val Ser Cys Ser Asn Asn Ile Gln Val Leu Asn Gly Ile Gln
         1155   1160   1165

Asn Ile Gly Ser Lys His Gln Pro Leu His Ser Ser Ile Ser Tyr His
     1170   1175   1180

Gln Thr Gly Gln Val His Leu Pro Asp Ile Val His Ala Ser Asp Leu
1185   1190   1195   1200

Glu Gln Ser Val Tyr Thr Gly Leu Asn Arg Val Leu Asp Ser Asn Val
              1205   1210   1215

Thr Gln Thr Ser Tyr Tyr Pro Ser Pro His Pro Gly Ile Ala Cys Asn
              1220   1225   1230

Asn Glu Thr Gln Lys Ala Asp Ser Leu Ser Asn Met Leu Tyr Gly Ile
         1235   1240   1245

Asp Arg Ser Asp Lys Thr Thr Ser Leu Ser Glu Pro Thr Pro Arg Ile
     1250   1255   1260

Asp Asn Cys Phe Gln Pro Leu Ser Ser Glu Lys Met Ser Phe Ala Arg
1265   1270   1275   1280

Glu Gln Ser Ser Ser Glu Asn Tyr Leu Ser Arg Asn Glu Ala Glu Ala
              1285   1290   1295

Ala Phe Val Lys Gln His Gly Thr Ser Asn Val Gln Gly Asp Asn Thr
              1300   1305   1310

Val Arg Thr Glu Gln Asn Gly Gly Glu Asn Ser Gln Ser Gly Tyr Ser
         1315   1320   1325

Gln Gln Asp Asp Asn Val Gly Phe Gln Thr Ala Thr Thr Ser Asn Leu
     1330   1335   1340

Tyr Ser Ser Asn Leu Cys Gln Asn Gln Lys Ala Asn Ser Glu Val Leu
1345   1350   1355   1360

His Gly Val Ser Ser Asn Leu Ile Glu Asn Ser Lys Asp Asp Lys Lys
              1365   1370   1375

Thr Ser Pro Lys Val Pro Val Asp Gly Ser Lys Ala Lys Arg Pro Arg
         1380   1385   1390

Val Gly Ala Gly Lys Lys Lys Thr Tyr Asp Trp Asp Met Leu Arg Lys
         1395   1400   1405

Glu Val Leu Tyr Ser His Gly Asn Lys Glu Arg Ser Gln Asn Ala Lys
     1410   1415   1420

46

Asp Ser Ile Asp Trp Glu Thr, Ile Arg Gln Ala Glu Val Lys Glu Ile
1425   1430   1435   1440

Ser Asp Thr Ile Arg Glu Arg Gly Met Asn Asn Met Leu Ala Glu Arg
                1445   1450   1455

Ile Lys Asp Phe Leu Asn Arg Leu Val Arg Asp His Gly Ser Ile Asp
            1460   1465   1470

Leu Glu Trp Leu Arg Tyr Val Asp Ser Asp Lys Ala Lys Asp Tyr Leu
            1475   1480   1485

Leu Ser Ile Arg Gly Leu Gly Leu Lys Ser Val Glu Cys Val Arg Leu
        1490   1495   1500

Leu Thr Leu His His Met Ala Phe Pro Val Asp Thr Asn Val Gly Arg
1505   1510   1515   .   1520

Ile Cys Val Arg Leu Gly Trp Val Pro Leu Gln Pro Leu Pro Glu Ser
            1525   1530   1535

Leu Gln Leu His Leu Leu Glu Met Tyr Pro Met Leu Glu Asn Ile Gln
        1540   1545   1550

Lys Tyr Leu Trp Pro Arg Leu Cys Lys Leu Asp Gln Arg Thr Leu Tyr
        1555   1560   1565

Glu Leu His Tyr Gln Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys
        1570   1575   1580

Ser Lys Pro Asn Cys Asn Ala Cys Pro Met Arg Ala Glu Cys Lys His
1585   1590   ` 1595   1600

Phe Ala Ser Ala Phe Ala Ser Ala Arg Leu Ala Leu Pro Gly Pro Glu
            1605   1610   1615

Glu Lys Ser Leu Val Thr Ser Gly Thr Pro Ile Ala Ala Glu Thr Phe
            1620   1625   1630

His Gln Thr Tyr Ile Ser Ser Arg Pro Val Val Ser Gln Leu Glu Trp
        1635   1640   1645

Asn Ser Asn Thr Cys His His Gly Met Asn Asn Arg Gln Pro Ile Ile
    1650   1655   1660

Glu Glu Pro Ala Ser Pro Glu Pro Glu His Glu Thr Glu Glu Met Lys
1665   1670   1675   1680

Glu Cys Ala Ile Glu Asp Ser Phe Val Asp Asp Pro Glu Glu Ile Pro
            1685   1690   1695

Thr Ile Lys Leu Asn Phe Glu Glu Phe Thr Gln Asn Leu Lys Ser Tyr
        1700   1705   1710

Met Gln Ala Asn Asn Ile Glu Ile Glu Asp Ala Asp Met Ser Lys Ala
        1715   1720   1725

Leu Val Ala Ile Thr Pro Glu Val Ala Ser Ile Pro Thr Pro Lys Leu
    1730   1735   1740

47

Lys Asn Val Ser Arg Leu Arg Thr Glu His Gln Val Tyr Glu Leu Pro
1745   1750   1755   1760

Asp Ser His Pro Leu Leu Glu Gly Phe Asn Gln Arg Glu Pro Asp Asp
                1765   1770   1775

Pro Cys Pro Tyr Leu Leu Ser Ile Trp Thr Pro Gly Glu Thr Ala Gln
            1780   1785   1790

Ser Thr Asp Ala Pro Lys Ser Val Cys Asn Ser Gln Glu Asn Gly Glu
            1795   1800   1805

Leu Cys Ala Ser Asn Thr Cys Phe Ser Cys Asn Ser Ile Arg Glu Ala
        1810   1815   1820

Gln Ala Gln Lys Val Arg Gly Thr Leu Leu Ile Pro Cys Arg Thr Ala
1825   1830   1835   1840

Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu
            1845   1850   1855

Val Phe Ala Asp His Asp Ser Ser Arg Asn Pro Ile Asp Val Pro Arg
        1860   1865   1870

Ser Trp Ile Trp Asn Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser
        1875   1880   1885

Ile Pro Thr Ile Phe Lys Gly Leu Thr Thr Glu Glu Ile Gln His Cys
        1890   1895   1900

Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg Thr Ser Arg
1905   1910   1915   1920

Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro Ala Ser Lys Ile
            1925   1930   1935

Thr Arg Asn Lys Lys Ser Ala Gly Ser Ala Pro Gly Arg Asp Asp Glu
            1940   1945   1950

<210> 18
<211> 723
<212> PRT
<213> Oryza sativa

<220>
<223> DMTRICE novel amino terminus

<400> 18
Met Gln Asp Phe Gly Gln Trp Leu Pro Gln Ser Gln Thr Thr Ala Asp
    1   5   10   15

Leu Tyr Phe Ser Ser Ile Pro Ile Pro Ser Gln Phe Asp Thr Ser Ile
            20   25   30

Glu Thr Gln Thr Arg Thr Ser Ala Val Val Ser Ser Glu Lys Glu Ser
        35   40   45

48

```
Ala Asn Ser Phe Val Pro His Asn Gly Thr Gly Leu Val Glu Arg Ile
    50                  55              60
Ser Asn Asp Ala Gly Leu Thr Glu Val Val Gly Ser Ser Ala Gly Pro
65                  70              75                      80
Thr Glu Cys Ile Asp Leu Asn Lys Thr Pro Ala Arg Lys Pro Lys Lys
                85              90                      95
Lys Lys His Arg Pro Lys Val Leu Lys Asp Asp Lys Pro Ser Lys Thr
            100             105             110
Pro Lys Ser Ala Thr Pro Ile Pro Ser Thr Glu Lys Val Glu Lys Pro
        115             120             125
Ser Gly Lys Arg Lys Tyr Val Arg Lys Lys Thr Ser Pro Gly Gln Pro
    130             135             140
Pro Ala Glu Gln Ala Ala Ser Ser His Cys Arg Ser Glu Leu Lys Ser
145             150             155                     160
Val Lys Arg Ser Leu Asp Phe Gly Gly Glu Val Leu Gln Glu Ser Thr
            165             170             175
Gln Ser Gly Ser Gln Val Pro Val Ala Glu Ile Cys Thr Gly Pro Lys
    180             185             190
Arg Gln Ser Ile Pro Ser Thr Ile Gln Arg Asp Ser Gln Ser Gln Leu
    195             200             205
Ala Cys His Val Val Ser Ser Thr Ser Ser Ile His Thr Ser Ala Ser
    210             215             220
Gln Met Val Asn Ala His Leu Phe Pro Pro Asp Asn Met Pro Asn Gly
225             230             235                     240
Val Leu Leu Asp Leu Asn Asn Ser Thr Ser Gln Leu Gln Asn Glu His
            245             250                     255
Ala Lys Phe Val Asp Ser Pro Ala Arg Leu Phe Gly Ser Arg Ile Arg
    260             265             270
Gln Thr Ser Gly Lys Asn Ser Leu Leu Glu Ile Tyr Ala Gly Met Ser
    275             280             285
Asp Arg Asn Val Pro Asp Leu Asn Ser Ser Ile Ser Gln Thr His Ser
    290             295             300
Met Ser Thr Asp Phe Ala Gln Tyr Leu Leu Ser Ser Ser Gln Ala Ser
305             310             315                     320
Val Arg Glu Thr Gln Met Ala Asn Gln Met Leu Asn Gly His Arg Met
            325             330             335
Pro Glu Asn Pro Ile Thr Pro Ser His Cys Ile Glu Arg Ala Ala Leu
            340             345             350
Lys Glu His Leu Asn His Val Pro His Ala Lys Ala Ala Val Met Asn
    355             360             365
```

49

```
Gly Gln Met Pro His Ser Tyr Arg Leu Ala Gln Asn Pro Ile Leu Pro
    370             375         380
Pro Asn His Ile Glu Gly Tyr Gln Val Met Glu Asn Leu Ser Glu Leu
385             390         395             400
Val Thr Thr Asn Asp Tyr Leu Thr Ala Ser Pro Phe Ser Gln Thr Gly
            405         410             415
Ala Ala Asn Arg Gln His Asn Ile Gly Asp Ser Met His Ile His Ala
        420         425             430
Leu Asp Pro Arg Arg Glu Ser Asn Ala Ser Ser Gly Ser Trp Ile Ser
        435             440             445
Leu Gly Val Asn Phe Asn Gln Gln Asn Asn Gly Trp Ala Ser Ala Gly
    450             455             460
Ala Ala Asp Ala Ala Ser Ser His Ala Pro Tyr Phe Ser Glu Pro His
465             470             475             480
Lys Arg Met Arg Thr Ala Tyr Leu Asn Asn Tyr Pro Asn Gly Val Val
            485             490             495
Gly His Phe Ser Thr Ser Ser Thr Asp Leu Ser Asn Asn Glu Asn Glu
        500             505             510
Asn Val Ala Ser Ala Ile Asn Ser Asn Val Phe Thr Leu Ala Asp Ala
        515             520             525
Gln Arg Leu Ile Ala Arg Glu Lys Ser Arg Ala Ser Gln Arg Met Ile
    530             535             540
Ser Phe Arg Ser Ser Lys Asn Asp Met Val Asn Arg Ser Glu Met Val
545             550             555             560
His Gln His Gly Arg Pro Ala Pro His Gly Ser Ala Cys Arg Glu Ser
            565             570             575
Ile Glu Val Pro Asp Lys Gln Phe Gly Leu Met Thr Glu Glu Leu Thr
            580             585             590
Gln Leu Pro Ser Met Pro Asn Asn Pro Gln Arg Glu Lys Tyr Ile Pro
    595             600             605
Gln Thr Gly Ser Cys Gln Leu Gln Ser Leu Glu His Asp Met Val Lys
    610             615             620
Gly His Asn Leu Ala Gly Glu Leu His Lys Gln Val Thr Ser Pro Gln
625             630             635             640
Val Val Ile Gln Ser Asn Phe Cys Val Thr Pro Pro Asp Val Leu Gly
            645             650             655
Arg Arg Thr Ser Gly Glu His Leu Arg Thr Leu Ile Ala Pro Thr His
        660             665             670
Ala Ser Thr Cys Lys Asp Thr Leu Lys Ala Leu Ser Cys Gln Leu Glu
        675             680             685
```

Ser Ser Arg Asp Ile Ile Arg Pro Pro Val Asn Pro Ile Gly Pro Ser
    690   695   700

Ser Ala Asp Val Pro Arg Thr Asp Asn His Gln Val Lys Val Ser Glu
705   710   715   720

Glu Thr Val

<210> 19
<211> 12120
<212> DNA
<213> Oryza sativa

<220>
<223> DMTRICE sequence from PAC P0489G09

<400> 19
aaatattgct taaatggata taaagttgaa aaatgtactt gagggaagtt gtaggtgcac 60
gtggggtccc acaatttttc ttcactagtg cacctttagt tatatatttt ttgcgcaaga 120
ggacaaaggc gctccgtgta attttgagta agggccggcg ggatatttat ttgtgtaaag 180
gacctagcca agaaaagcat gatagtgcat atgtatcctt tcttttttctt ttcttttgtt 240
ttcataactg tcttacagaa tttcatgttg gctggtgaca cttgtctcac tcattatttg 300
gtatattttg actaaatgca acgtgttggt gctcggtagt ttatatttgt ttttacgcat 360
tcttcattga ctgtatgtat ttgatgttga taccctgggc tgtcttattt tataggtgga 420
tgctgggagg ccacatagga ggcctgtgtg atccaagtgt gctgctcctg agttgaaatt 480
gcatagccat atagcaacta ctggtgtaaa cttgagagat gaagtagtga aaggaaatat 540
gcaggatttt ggacaatggc tgcctcaatc tcagaccact gccgatctat atttctccag 600
tattccaata ccatcacagt tcgatacttc catagagacg cagactagaa cttctgcagt 660
tgtatcgtca gagaaagaat ctgctaattc gttcgtccct cataatggta ctgggcttgt 720
tgaacgcatt agcaatgatg ctgggctaac tgaagtagtt ggaagtagtg ctggaccaac 780
tgaatgtatt gacttgaaca agacaccagc acggaaaccc aagaagaaaa agcacaggcc 840
aaaggtgcta aaggacgata aaccatcgaa gacacctaaa tctgctactc caataccttc 900
aacagaaaag gtagaaaaac catctggaaa gagaaaatat gtccgcaaga agacatctcc 960
aggccaacct cctgcagaac aggcagctag ctcacactgc agatctgagc tgaagtcagt 1020
taaacgaagt ttggactttg gtggagaagt actgcaagag agtacacaat ctggatctca 1080
agttccggtg gcagaaatat gtactggtcc caagcgtcaa tcaatacctt ctaccatcca 1140
aagagattcg caaagccagt tggcttgcca cgtggtttct agcaccagct caattcacac 1200
ttcagctagt cagatggtta atgcacattt gtttcctcct gataacatgc caaatggagt 1260
attgcttgac ctcaataatt ctactagtca gttacaaaac gaacatgcta aatttgtgga 1320
cagtccggca cgtctttttg gttccagaat aagacagaca tcaggtaaaa attctttgct 1380
agaaatctat gctggcatgt cagatagaaa tgtacctgat ctcaacagtt caatcagtca 1440
gacgcatagc atgtctactg attttgctca atacttgctt tcatcctcac aagcttctgt 1500
aagggaaaca caaatggcca atcagatgct taatggtcat aggatgccag aaaatccaat 1560
tacacctagt cattgtattg aaagggctgc attgaaggaa catttgaatc atgttcctca 1620
cgcaaaagcc gcagtgatga atggccaaat gccccatagt tacaggttgg cgcaaaatcc 1680
catcctacct ccaaatcata ttgaagggta tcaagtgatg gaaaatttga gtgaacttgt 1740
cacgacaaat gactatctaa ctgctagtcc tttcagtcaa actggagctg caaataggca 1800
gcataatatt ggtgactcca tgcatataca tgcattggat cctagaagag agagtaatgc 1860
ttcaagtggt tcttggatat cattaggtgt gaactttaac caacaaaata atggatgggc 1920
atctgcaggt gctgccgatg ctgcgagctc acatgcccca tattttcag aacctcacaa 1980
aagaatgagg acagcttatc ttaacaatta tccaaatgga gtcgtgggac atttttctac 2040
ctcatctacg gatttgtcaa ataatgagaa tgaaaatgtg gcctcagcaa tcaactcaaa 2100
cgtttttacc cttgctgatg cacaaagatt gatagcccgt gagaaatcac gagcttccca 2160
aagaatgatc agttttagat catctaaaaa tgatatggtt aacagatcag aaatggtcca 2220
tcaacatggc agacctgctc cgcatggctc tgcatgcagg gagtctattg aagtacctga 2280
caaacagttc gggctcatga cagaagaact cacacaatta cctagtatgc caaataaccc 2340
acaaagggaa aaatatattc cgcaaactgg aagttgccaa cttcagtctt tggaacatga 2400
catggttaaa gggcataact ggcaggtga attgcataag caagtaactt cacctcaagt 2460
tgttattcag agcaatttct gtgttacccc tcctgatgtg ctcggcagaa gaaccagtgg 2520

51

```
ggagcattta agaacccTta tagctccaac acatgcatcg acatgtaagg acactctgaa 2580
agctttaagt tgtcaactgg agagttctag agacattatt aggcctcctg tcaatcctat 2640
agggccatcc tctgccgatg ttccaagaac tgataaccat caagtcaagg tttctgaaga 2700
aaccgttaca gccaaactcc ctgagaagcg aaaagtagga cgtcccagaa aagagttaaa 2760
acctggtgag aaaccaaaac ctagaggccg tccaaggaag ggaaaagttg ttggtggaga 2820
acttgcatca aaggatagtc acactaatcc attgcaaaat gagagtactt catgttctta 2880
tggtccttat gcaggggagg cttctgttgg aagagcagtt aaagcaaata gagttggaga 2940
aaacatttct ggagctatgg tatccctact ggattcttta gatattgtta ttcaaaagat 3000
aaaggtcttg gacataaaca aatcagaaga ccctgtgaca gctgaacctc atggtgctct 3060
tgtcccttac aatggagaat ttggtcctat tgttcctttt gaggggaaag tgaaaagaaa 3120
acgctctcga gccaaagtgg atcttgaccc tgtaactgct ttaatgtgga agttactaat 3180
gggaccagat atgagtgatt gtgctgaagg tatggataag gataaagaga aatggctaaa 3240
tgaagaaaga aaaatattcc aagggcgtgt tgattcattt attgctcgaa tgcatctagt 3300
tcaaggtatt tctatcattt taaaattgtt ttcctaacat gaacatgatg gcttccatct 3360
tgtgattgct gccctcacat tagtgaatgg tctcaaatct tcaatattta ctgtgtaccc 3420
aaatcctatt tcttcatccc aatatattca tgtttgtact cgtactgtcc cattagactt 3480
gcattgtgct gtgaagatca acacctttac ttttaggatt acctctatgt ttgcaggaga 3540
tcggcgtttt tctccttgga aaggatcagt tgtagattct gtagtgggag tatttcttac 3600
acagaatgtt tcggaccatc tttccaggtg aataatgcct agagcctatt tgaaaactgt 3660
gacttgactt gcattgtgag gttatgttgt ttttctgtct gactatttcc tttttttca 3720
gctctgcatt tatggctctt gctgcaaaat ttcctgtaaa gccagaagcc tctgaaaaac 3780
ccgcaaatgt gatgtttcat acaatttcag aaaatggtga ttgttctggg ttgtttggta 3840
attctgtcaa gctacagggt gagatccttg ttcaggaggc cagcaacaca gcagcctctt 3900
ttatcacaac cgaggataag gaaggaagta acagtgtgga attgcttgga agttcttttg 3960
gggatggagt ggatggtgca gcaggagttt attctaatat ttatgagaat ctgccagcta 4020
gactgcatgc tactaggcgt ccagtcgttc aaactggaaa cgctgtcgaa gcggaagatg 4080
ggtcactgga gggtgttgtt tcatcagaaa actccactat ttcatctcaa aattcatcag 4140
attatctatt tcacatgtct gatcatatgt tttcgagcat gttactaaat ttcactgccg 4200
aagacattgg cagcagaaat atgcccaaag caacaagaac cacatataca gaacttctac 4260
gaatgcagga gctgaagaac aagtctaatg aaaccattga atcatcagag tatcatgggg 4320
ttccagtctc atgtagtaac aacattcaag tgctcaatgg aatacaaaat atcggcagta 4380
aacatcagcc tttacattcc tctatttcat atcaccagac tggccaagtt cacctcccag 4440
acatagtaca tgcgagtgat ttggagcaat cagtatacac tggccttaat agagtgcttg 4500
attctaatgt tacacaaacc agttattatc cttcacctca tcctggaatt gcctgtaaca 4560
atgaaacaca aaaggctgac tctttaagca acatgttata tggtatagat agatcagata 4620
agactacttc cctgtctgag cctacaccaa gaatcgataa ctgttttcaa ccattaagtt 4680
cagagaaaat gtcatttgct agggaacagt cctcttctga aaattatctt tcaaggaatg 4740
aagctgaagc tgcatttgtt aaacagcatg gaacatcaaa tgtgcaaggt gataatactg 4800
tcaggacaga gcaaaatgga ggtgaaaatt ctcaatcagg atacagccaa caggatgata 4860
atgttggatt tcaaacagcg acaaccagta atctttattc ttcaaactta tgccaaaacc 4920
agaaagcaaa ttctgaagta ctacacggag tttcttccaa cttgatagag aattctaaag 4980
atgacaaaaa gacttccccc aaagttccag tcgatggatc aaaagcaaag aggccaagag 5040
ttggggctgg taaaaagaaa acatatgatt gggatatgtt gagaaagaa gttctttaca 5100
gtcatggtaa taaagaaaga tcccagaatg ctaaggactc aattgattgg gaaacaataa 5160
gacaagcaga ggtgaaggaa atatctgaca caattagaga gcgaggaatg aataacatgc 5220
tggcagaacg gataaaagta agtatggcat aaaacagttt acattgaaag ttgacataac 5280
tctagtcata tgtgcatgca tgctattcca tatagatttg cttatttgtt ggaattccaa 5340
gttttggatc aaccatactc atctttagca attcatgttg caggacttcc taaaccgatt 5400
ggtgagagac catgggagca tcgatcttga gtggttgcgc tatgtcgatt cagataaagc 5460
gaagtaagct aactaaattt attttgagca aacattcata atgcaattgg cccttgggca 5520
ttctataatt tgtcattttg acctctgcat tgcttagcaa tgacaattgg atgtagtgag 5580
catgggtaat aatgtaagca atgacaattg gatgtagtgg gcatggttaa taattgaaca 5640
tgtctgtgtt tgcgggataa taatgcctat cacctgtgag cctgtgacat gcaaaccttg 5700
aacgttgaac cttgaacccc ctacctcgca ctgtgtgctc tcaaccaact gagcaagtga 5760
gggaccttgt tgtatggaaa aaataatttt aaataaccct tgattcaacc aaagcttcat 5820
aaaagaatat attttctatt attcatttga accagcggtt gaaccagtga accgatggtc 5880
ttgctggtcc ggatttaata ataactatgg ctagaacaga ttagagcacc gaatacttgc 5940
gcgatgctaa atatttcaat ggggacacac ctgctcgtgt gttgcatcaa ctacctaagc 6000
cacacaggca tggcaatcaa atcagcttgc ccatgtaaca tcaactatct gatcgcgaga 6060
aggccggagc tctcacttga tgtttgtcat tcaaaaaata gttattcacc aatgcaatgt 6120
caagctcccg taaagaccat gaatgtagtt tatccttctt tgatcaagtt tttatttata 6180
```

52

```
ttaaagtgtt taccaatgta atcctacatt atttgtacct ggttttttaca tataaataca 6240
ttgtacctttt tgtgtttctt ccagggacta tctcttaagc attagaggac ttggacttaa 6300
aagtgttgag tgtgtgcgtc ttttgacact ccatcacatg gcttttcctg tatgtttcct 6360
ttcacaaata attttcaaga atcttcgttt ctttatttct ggagaagtgg agattttatc 6420
tgtatctgtt gatgatgtag gtggatacaa atgttggtag aatatgtgtg aggcttggat 6480
gggtgccact tcagcccta cccgagtctc ttcagttgca cctgttggag atgtaagtat 6540
cttaaatcca ctggttggct tcactaatgc tggagagtga taggagtttg atcatctgct 6600
attgaaggta tccaatgctg gagaacatac agaaatacct ctggccgagg ttatgcaagc 6660
ttgatcaacg gacattgtga gtttttagaaa tgcagttaaa aactatatat ataagagcat 6720
gtcattatct gagagtgtat aacaggttct tgatgatatg taggtatgag cttcactatc 6780
aaatgataac ttttggaaag gtatgagaca acaactttga taaagtgaat tcaacccaat 6840
tactgtgttt tgatggacca tctgtgttac tttccttcta ggtattttgt acaaaaagta 6900
agcccaattg caacgcatgc ccaatgagag ctgagtgcaa gcactttgca agtgcatttg 6960
ccaggtaatt ctcaagatgt acatatttta tatacattct gtgaaatcac ggtgatgatt 7020
gttaggtatg aacaattggc tgagatcccc cccctccccc ctcccatcct tttcctggtc 7080
ctacaagttc tcctaggcta atttaactgg tgcataccac atttatgtta ttttgataca 7140
tcaaagatta tgtttgtggt tgtgaggcta tattagtgtg ttgtatgtaa ctcagttttg 7200
caattgtagt tttagttaga acacgttgtt ctctacattt taataaatac ttttttgactg 7260
gacatcaatg actggtgtat ttccgatata aaaaggttga ttgttgccga gggatttcaa 7320
ttcggtccga ataggttcga caaatgcagt gggcctatta gtttaagagt gaaagttcta 7380
tcagctgttt gactccactg tgacctttac actttgtact tttgaagaaa cagactaacc 7440
tgctcatatt aaagtcttgg aatgactcca ttgcgacctt tacgctttgt attttagaag 7500
aaacagacta acctgttcat attagagtct tggaactgtg tgtgtgtgtg tttttttttt 7560
ttttggggggg gggggggcat ggagatttaa tccaacattc ctggatgacc ttatattggt 7620
aatgatatgg ttttttttatg atatagtgca aggctcgctc ttcctggacc tgaagagaag 7680
agtttagtta catctggaac cccaatagct gcagaaacct tccaccagac atatataagt 7740
tctaggcctg tagtaagtca gcttgagtgg aattcaaaca cctgtcacca tggtatgaac 7800
aatcgccagc caatcattga ggagccagca agcccagaac ctgaacatga gacagaagag 7860
atgaaagagt gtgcaataga ggatagtttt gtcgatgatc cagaagaaat ccctactatc 7920
aagcttaatt ttgaggagtt tacacagaac ctgaagagtt atatgcaagc aaataacatt 7980
gagattgaag atgctgatat gtcaaaggct ttggtcgcta taactcctga agttgcttct 8040
atcccaactc ctaagctcaa gaatgtcagt cgcctaagga cagagcacca agtgtatgat 8100
cttgtccctc ttgcaaaacc aatctcatga atatttacta ttgactatca tgtgttttgc 8160
tgcattgctt acttctctgt tttcaacata tatgtagcta tgaactgcca gattcacatc 8220
cacttcttga aggagtaagt tcataaaaca ttatagaatt ctgtactttc cttatcacca 8280
actgagaata tattgatgct tattttctta caatacacag ttcaaccaaa gagaaccaga 8340
tgatccttgc ccatacctac tctctatatg gaccccaggt aagaagtgca taaacagaac 8400
acaatatcat gggaaccaaa ctttttttcaa tggttactta taattgttga aatatgcaac 8460
aggtgaaaca gctcaatcaa ctgatgcacc taagtcggtc tgcaattcac aagagaatgg 8520
tgaactatgt gcaagcaata catgctttag ttgcaacagt ataagagaag cgcaggccca 8580
aaaagttcga gggacactgc tggtaagtag ttgtttctgt aacatatgct cagttgccct 8640
tggttcaaga tgtgctattc aagtttatca tgttcacgaa tagtgataaa gctgctatct 8700
gtcctagcta ttgtccaagc tataacagtt ctgattcact ggttgggcac cagctaggga 8760
ataggatgta aaaaacttat cccgcagttt gttgacaatc tgttttttctt tgttgaaaat 8820
taaaaataga taccatgccg aacagcaatg agaggaagct ttccacttaa tgggacatat 8880
tttcaagtca atgaggtgaa aacagaaagt tcttaaagtt gatcttagtt taattattat 8940
aataccatta aaatatatgc aagtttctac tttctagtat ctcttttatt agtgttcaaa 9000
tgttatgcgg caggtatttg ctgatcatga ctcaagccgg aacccgattg atgttccaag 9060
gagttggata tggaatctcc ctaggagaac tgtttacttt ggaacttcaa ttccgacaat 9120
atttaaaggt atttcactaa taaattttga ccaagaatag gattttttggc agcgccaaat 9180
gtgccactat ctttattgtg tgaagtccat tatgtgattg taataatttg aatcaccaag 9240
aggactaagg cctgctttgg gacatattac gagcagcttt gcttgcaaa gaaaccagat 9300
tctggtgccg caccttctcc gctcttctgc cacccaagtc cgtccaatac ccctcattga 9360
gcgcttggat cctaacccca tctgccatca tgcatcatcc tgctaacaac tgcttccacc 9420
attgcctgtt tctgttgttg ggaggcactc acgctgcttg ctatagttta ggttttcttt 9480
gtgtcctgat ttagatggaa tttccagctg ctgtctttta cataactagc taaatgtccg 9540
cgctttgcta tggataatag aaaatatatt ataatattgt caaataaatt aaatatgttt 9600
tatacgaaat gtgttaacaa tccttttgct atagggaata ttgaccttaa tttgatttta 9660
tatgtggcta tccatttaga tttgtttgtt tttctaataa taataagttc aagggctaat 9720
gtacaaaatt gacaatggga gtaggtgggg tggcagattc actgccacca ccactacctt 9780
cttttaaagg ggtatataga tttgcagcag tggttgcttg atctgtgatt tgaaatgtca 9840
```

53

```
agtacacgct catgcatcag caccatatgt ctacgctcct gacccaacat gcaaccaatg 9900
caattgaggg ttggctctga tacaattact aatgtcctat atccaaaaca actataggcc 9960
tatgaccaaa cataattaat aacctcgctt gcgctttttgt cctcacttgc tccatgtaaa 10020
agggttaacc cgaggttact atgttaggaa tagctgggtt tatgaaacgg ttcaactctc 10080
aactcctcat atagcactaa ttcatgtatt gctgtcagca gtgatttgag ttccagatca 10140
tgctcataag ataggaccaa attgtcctta ctatctactc cctccgtccc aaaatataag 10200
gtatttccgg tcaaaatatc ttatattttg ggatggaggg agtactatac tacggaccca 10260
ccaccaaata gtgccgcaga agagagagag agagagagaa gaggggggtgg gggtgggggt 10320
gtatgggtga aataagaata gtgccaagta tttgccaaca aatgaggcgg tcaaatgtgt 10380
cacatcaatt gggaagtatg tcagatcaac tgaaaatttg attgggaaat tattattcat 10440
gcaacaaagc tgtacaactg atcccatgtt tctatcgcag gtttgacaac tgaagaaata 10500
caacattgct tttggagagg taatcatttt tttttgtatg tacgttttgg tttccataac 10560
aaagagagat gaagtgtata ggtactatgt ttactgacaa ggataataat agtagcaagt 10620
atataggcag aggagcatgt ctctattcta ccagtattat tactcataat aactagtata 10680
tcctttttt tgccatttca gctgatagct actctccagt caaaatattt gccatctcta 10740
ttgaactttt cattgtcttc tgaatgtatc ttactcttgg atcattaata tttcattttg 10800
tcacgatata gtggtatagg acaataaaat catgggaagt atttattttc atcaccaatc 10860
tactcatata attttcaaat gacaattata aatatcttaa aaatatattg ttagttgtcc 10920
tgtataaaat aattgtcaca ccctagtcca cagcgacaag aatttgtgtc tacaggctag 10980
agtgagtact ctagaagtat cttcatagga atcggaataa aatgccaatg tgaatgaaca 11040
aggatatcaa gtataccctc aaaatctcta gagaggattg cgtaaatatg taggtgtaat 11100
taaacaattg tttcatatgg agggttttct taaaggaggt acaagactta tcaatatggg 11160
taaagtagtt tttatccata ggcattgttg cagaaagct gcttagggta gaatgctact 11220
ccctccgtcc cacaatataa gagatttga gtttttgctt gcaacgtttg accactcggc 11280
ttattcaaaa attttgaaa ttattattta ttttatttgt gacttacttt attattcaca 11340
gtactttaag tacaactttt cgttttttat atttgcaaaa aaaattgtat aagacgagtg 11400
gtcaaacgtt gtacgcaaaa actcaaaatc ccttatattg tgggacggag ggagtactta 11460
tggatgcctt ttttgtccaa gatgtcagta acatttctt tcagggatgt ggattttac 11520
ttcttttttc cctaactttt tcaggatttg tgtgcgtgag aggctttgat aggacatcaa 11580
gagcacccag accactgtat gcaagactcc actttccagc aagcaaaat accaggaata 11640
aaaaatctgc aggttctgct ccaggaagag atgatgaata ggccatctgg aaaaccagaa 11700
aggaaataaa gaggaggtac atatgatctg ccagaagatc actgacctga aatggatcgc 11760
tgaccaataa gttgccgtag caattcaat tatttctggc catatacatc tgctgaaagt 11820
tatgaactcc agccactgac gaattcgtgg tgctggtatt cttcggcaac atgatccatc 11880
atacagattc tatgcttggt tgttgcaagc aattcttatg cggtgacagt tgctgctgat 11940
agggagaaaa ggcatgtccg gcggctcagc ggctctaact gtactttcat atgagtggaa 12000
ccgattgttg tacatgtgaa aagtttgcca ttcaaaatgg tcattcatgt tgttaggtca 12060
ttcatgtagt cgatgtcaaa ttaatcatca attatttgat ttgattcatt cacaagttta 12120
```

<210> 20
<211> 177
<212> PRT
<213> Zea mays

<220>
<223> corn DMT.1 660990 (688512 selclone ID)

<400> 20
Glu Pro Asp Asp Pro Cys Pro Tyr Leu Leu Ser Ile Trp Thr Pro Gly
1   5   10   15

Glu Thr Ala Gln Ser Ile Asp Ala Pro Lys Thr Phe Cys Asp Ser Gly
            20   25   30

Glu Thr Gly Arg Leu Cys Gly Ser Ser Thr Cys Phe Ser Cys Asn Asn
        35   40   45

Ile Arg Glu Met Gln Ala Gln Lys Val Arg Gly Thr Leu Leu Ile Pro
    50   55   60

54

```
Cys Arg Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe
65              70              75              80

Gln Val Asn Glu Val Phe Ala Asp His Cys Ser Ser Gln Asn Pro Ile
                85              90              95

Asp Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val Tyr
            100             105             110

Phe Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu Glu
        115             120             125

Ile Gln Arg Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp
    130             135             140

Arg Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro
145             150             155             160

Val Ser Lys Val Val Arg Gly Lys Lys Pro Gly Ala Ala Arg Ala Glu
                165             170             175

Glu


<210> 21
<211> 798
<212> DNA
<213> Zea mays

<220>
<223> corn DMT.1 cDNA 660990 (668512 selclone ID)

<400> 21
gaaccagatg atccttgtcc atatcttctt tccatatgga ccccaggtga aactgcacaa 60
tcgatcgatg cccccaagac attctgtgat tcaggggaga cgggtagact atgtggaagt 120
tcaacatgct ttagttgcaa caatatacga gaaatgcagg ctcagaaagt cagaggaaca 180
cttttgatac catgccgaac agcaatgaga ggaagcttcc cacttaatgg gacgtatttt 240
caagttaatg aggtatttgc tgaccattgc tcaagtcaaa atccaattga tgtcccacga 300
agttggattt gggacctccc aagacgaact gtttactttg gaacctcagt tcctacaata 360
ttcagaggtt taacgactga agagatacaa cgatgctttt ggagaggatt tgtttgcgtg 420
aggggctttg ataggacagt gcgggcacca aggccccttt atgcaaggtt gcattttcct 480
gtcagcaagg ttgttagagg caaaaagcct ggagcagcaa gagcagaaga ataatagaac 540
attgaagaaa tataggggtg ctaaccagat gaggatggat agcccgaaat gagatgctga 600
cccaataggt cgccaaatca cctccaaatt ctaacccaat gacttccatc tgtaatgaat 660
ggcaatacct tgaaaacctg tgatggagat gttttgtggc gacatgatct cttaaattag 720
attccgtctt tggtaacagc ctagctgttc ttgttgagtc gcatattctt tattctgaag 780
atcaatatag caaatggg                                                798


<210> 22
<211> 166
<212> PRT
<213> Zea mays

<220>
<223> corn DMT.2 371537 (441428 selclone ID)
```

<220>
<221> MOD_RES
<222> (1)..(166)
<223> Xaa = any amino acid

<400> 22
Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Arg Gln Pro Asn Cys
1   5   10   15

Asn Ala Cys Pro Met Arg Ser Glu Cys Lys His Phe Ala Ser Ala Phe
            20   25   30

Ala Ser Ala Arg Leu Ala Leu Pro Ala Pro Gln Glu Glu Ser Leu Val
        35   40   45

Lys Leu Ser Asn Pro Phe Ala Phe Gln Asn Ser Ser Met His Ala Met
    50   55   60

Asn Ser Thr His Leu Pro Arg Leu Glu Gly Ser Ile His Ser Arg Glu
65   70   75   80

Phe Leu Pro Lys Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro
                85   90   95

Arg Glu Glu Arg Pro Pro Xaa Thr Met Glu Asn Asp Ile Glu Asp Phe
            100   105   110

Tyr Glu Asp Gly Glu Ile Pro Thr Ile Lys Leu Asn Met Glu Ala Phe
        115   120   125

Ala Gln Asn Leu Glu Asn Cys Ile Lys Glu Ser Asn Asn Glu Leu Gln
    130   135   140

Ser Asp Asp Ile Ala Lys Ala Leu Val Ala Ile Xaa Thr Glu Xaa Ala
145   150   155   160

Ser Ile Pro Xaa Pro Lys
                165

<210> 23
<211> 506
<212> DNA
<213> Zea mays

<220>
<223> corn DMT.2 cDNA 371537 (441428 selclone ID)

<400> 23
tatcagatga ttacatttgg aaaggtcttt tgtaccaaaa gacagccaaa ttgcaatgca 60
tgcccaatga ggagtgagtg caagcatttt gcaagtgcat ttgcaagtgc aaggcttgca 120
cttcctgctc cccaggagga aagcttagtg aagttgagca atccatttgc tttccagaat 180
agcagcatgc atgctatgaa ttcgactcac ctacctcgcc ttgaggggag tatccattca 240
agggagtttc ttcctaagaa ctcagagcca ataatcgagg agcctgcaag tccaagagag 300
gaaagacctc cakaaaccat ggaaaatgat attgaagatt tttatgaaga tggtgaaatc 360
ccaacaataa agcttaacat ggaagctttt gcacaaaact tggagaattg cattaaagaa 420
agcaataacg aactccagtc tgatgatatt gcaaagcat tggttgctat tarcactgaa 480
rcagcttcsa ttcctgkacc gaaact   506

56

<210> 24
<211> 276
<212> PRT
<213> Zea mays

<220>
<223> corn DMT.3 218853

<400> 24
Met Pro Arg Lys Pro Lys Arg Lys Ala Pro Ala Ser Pro Ala Arg His
 1   5   10   15

Asp Pro Ser Pro Glu Pro Tyr Pro Ser His Ala Ser Pro Cys Ser Ala
            20   25   30

Gln Cys Leu Val Val Arg Asp Ala Leu Leu Ala Phe His Gly Phe Pro
        35   40   45

Glu Glu Phe Ala Ala Phe Arg Val Leu Arg Leu Gly Gly Leu Ser Pro
    50   55   60

Asn Arg Asp Pro Arg Pro Ser Ser Pro Thr Val Leu Asp Gly Leu Val
65   70   75   80

Thr Thr Leu Leu Ser Gln Asn Thr Thr Asp Ala Ile Ser Arg Arg Ala
            85   90   95

Phe Ala Ser Leu Lys Ala Ala Phe Pro Ser Trp Asp Gln Val Val Asp
        100   105   110

Glu Glu Gly Lys Arg Leu Glu Asp Ala Ile Arg Cys Gly Gly Leu Ala
        115   120   125

Ala Thr Lys Ala Ala Arg Ile Arg Ser Met Leu Arg Asp Val Arg Glu
    130   135   140

Arg Arg Gly Lys Ile Cys Leu Glu Tyr Leu Arg Glu Leu Ser Val Asp
145   150   155   160

Glu Val Lys Lys Glu Leu Ser Arg Phe Lys Gly Ile Gly Pro Lys Thr
                165   170   175

Val Ala Cys Val Leu Met Phe Tyr Leu Gln Lys Asp Asp Phe Pro Val
        180   185   190

Asp Thr His Val Leu Arg Ile Thr Lys Ala Met Gly Trp Val Pro Ala
        195   200   205

Thr Ala Ser Arg Glu Lys Ala Tyr Ile His Leu Asn Asn Lys Ile Pro
    210   215   220

Asp Asp Leu Lys Phe Asp Leu Asn Cys Leu Phe Val Thr His Gly Lys
225   230   235   240

Leu Cys Gln Ser Cys Thr Lys Lys Val Gly Ser Asp Lys Arg Lys Ser
                245   250   255

Ser Asn Ser Ala Cys Pro Leu Ala Gly Tyr Cys Cys Ile Gly Glu Lys
                260   265   270

Leu Gln Gln Leu
        275

<210> 25
<211> 183
<212> PRT
<213> Triticum sp.

<220>
<223> wheat DMT.1 614028 (887053 selclone ID)

<400> 25
Met Arg Ala Glu Cys Lys His Phe Ala Ser Ala Phe Ala Ser Ala Arg
  1   5   10   15

Leu Ala Leu Pro Gly Pro Glu Glu Lys Ser Leu Val Thr Ser Gly Asn
              20   25   30

Pro Ile Ala Ser Gly Ser Cys Gln Gln Pro Tyr Ile Ser Ser Met Arg
          35   40   45

Leu Asn Gln Leu Asp Trp Asn Ala Asn Ala His Asp His Ile Leu Asp
      50   55   60

Asn Arg Gln Pro Ile Ile Glu Glu Pro Ala Ser Pro Glu Pro Glu Pro
 65   70   75   80

Glu Thr Ala Glu Met Arg Glu Ser Ala Ile Glu Asp Ile Phe Leu Asp
                  85   90   95

Asp Pro Glu Glu Ile Pro Thr Ile Lys Leu Asn Phe Glu Glu Phe Ala
              100   105   110

Gln Asn Leu Lys Asn Tyr Met Gln Val Asn Asn Ile Glu Met Glu Asp
          115   120   125

Ala Asp Met Ser Ser Ala Leu Val Ala Ile Thr Pro Glu Ala Ala Ser
      130   135   140

Ile Pro Thr Pro Arg Leu Lys Asn Val Ser Arg Leu Arg Thr Glu His
145   150   155   160

Gln Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Glu Gly Tyr Asp
                  165   170   175

Gln Arg Glu Pro Asp Asp Pro
              180

<210> 26
<211> 557
<212> DNA
<213> Triticum sp.

<220>
<223> wheat DMT.1 614028 (887053 selclone ID)

<400> 26
tgcccaatga gagctgaatg caagcacttt gcaagtgcat ttgcaagtgc tagacttgct 60
cttcctggac ctgaagagaa gagtttggtt acgtcaggaa acccaattgc ttcagggagc 120

58

```
tgccagcagc catacataag ttctatgcgt ttaaatcaac ttgactggaa tgcaaatgcc 180
catgaccata ttctggacaa tcgccagcca atcattgagg agccagcaag tccggaacca 240
gaaccagaga ctgcagagat gagagagagt gccatagagg atatttttct tgatgatcct 300
gaagaaattc ctacaatcaa gcttaatttc gaggagtttg cacagaatct caagaattat 360
atgcaagtca ataacattga aatggaagat gctgatatgt caagtgcctt ggttgccata 420
actccggaag ctgcatctat cccgactcct aggctcaaga atgttagtcg cctaagaaca 480
gagcatcaag tctatgaact gccggactca catccacttc tggaaggata cgaccaaaga 540
gagcctgatg atccttg                                              557
```

<210> 27
<211> 145
<212> PRT
<213> Triticum sp.

<220>
<223> wheat DMT.2 568842 (908118 selclone ID)

<400> 27

```
Asn Arg Val Asp Glu Ser Thr Val Gly Gly Ala Asp Lys Ala Ala Ser
  1               5                  10                  15

Pro Lys Lys Thr Arg Thr Thr Arg Lys Lys Asn Thr Glu Asn Phe Asp
             20                  25                  30

Trp Asp Lys Phe Arg Arg Gln Ala Cys Ala Asp Gly His Met Lys Glu
         35                  40                  45

Arg Lys Ser Glu Arg Arg Asp Ser Val Asp Trp Glu Ala Val Arg Cys
     50                  55                  60

Ala Asp Val Gln Arg Ile Ser Gln Ala Ile Arg Glu Arg Gly Met Asn
 65                  70                  75                  80

Asn Val Leu Ser Glu Arg Ile Gln Glu Phe Leu Asn Arg Leu Val Arg
                 85                  90                  95

Asp His Gly Ser Ile Asp Leu Glu Trp Leu Arg Asp Ile Pro Pro Asp
             100                 105                 110

Ser Ala Lys Asp Tyr Leu Leu Ser Ile Arg Gly Leu Gly Leu Lys Ser
             115                 120                 125

Val Glu Cys Val Arg Leu Leu Thr Leu His His Leu Ala Phe Pro Val
     130                 135                 140

Asp
145
```

<210> 28
<211> 439
<212> DNA
<213> Triticum sp.

<220>
<223> wheat DMT.2 568842 (908118 selclone ID)

<400> 28
```
caaacagggt ggatgaatct actgtcggag gagcagataa agcagcaagt ccaaagaaaa  60
caagaaccac aagaaaaaaa aatactgaaa acttcgactg gacaaatttt cgaagacagg 120
```

```
cctgtgctga tggccacatg aaagaaagga agtctgaaag aagagactct gttgattggg 180
aagcagtacg atgtgcagat gtacaaagaa tttctcaggc catccgggaa cgaggaatga 240
ataatgtttt atcagaacga atccaggaat tcctgaatcg cttggttaga gatcatggaa 300
gcattgatct tgaatggtta agagatatcc ccctgactc agcaaaggac tacttgctta 360
gcatacgtgg actggggctc aaaagtgttg aatgtgttcg tctactgaca ttacatcatc 420
tcgctttccc tgtwgacac                                          439
```

<210> 29
<211> 108
<212> PRT
<213> Triticum sp.

<220>
<223> wheat DMT.3 611792 (838515 selclone ID)

<400> 29
```
Asn Arg Lys Gln Val Asn Glu Val Phe Ala Asp His Lys Ser Ser Tyr
 1               5                  10              -      15

Asp Pro Ile Tyr Val Ala Arg Glu Gln Leu Trp Lys Leu Glu Arg Arg
             20                  25                  30

Met Val Tyr Phe Gly Thr Ser Val Pro Ser Ile Phe Lys Gly Leu Thr
         35                  40                  45

Thr Glu Glu Ile Gln Gln Cys Phe Trp Lys Gly Phe Val Cys Val Arg
     50                  55                  60

Gly Phe Glu Arg Glu Thr Gly Ala Pro Arg Pro Leu Cys Gln His Leu
 65                  70                  75                  80

His Val Ala Ala Ser Lys Val Pro Arg Ser Arg Asn Ala Ala Ala Ala
                 85                  90                  95

Gly Leu Asn Ser Asp Ser Ala Lys Ala Ser Ala Pro
             100                 105
```

<210> 30
<211> 624
<212> DNA
<213> Triticum sp.

<220>
<223> wheat DMT.3 611792 (838515 selclone ID)

<400> 30
```
aatcgaaaac aagttaatga ggtatttgca gaccacaaat ctagctacga tcccatatac 60
gttgcaaggg agcagttatg gaagttggaa agacgaatgg tctactttgg aacttcagtg 120
ccctccatat tcaaaggtct aacaactgaa gaaatacagc agtgcttctg aaaggattt 180
gtctgtgtgc ggggattcga gagggaaacc ggggcaccaa ggcctctatg ccaacatctg 240
cacgtcgcgg ctagcaaagt gccgagatca cgcaacgcgg cagcagctgg gctgaactcg 300
gattcagcaa aggcatcggc tccatgagta tcatcacacc ggctatcgac ctgtgcatgg 360
gtacgctagt gttggttcct gccgggcwac agccgttytt gtaggaaata aaccsctgcg 420
caaragaatt atcatccagt tggtytgagt gtatacttyt gctgtagkac cttttttaa 480
aatccctgtg agctytattg taccttgaat ttactttccg accagtttat ccgcttgcaa 540
araggccttt gttatgkacc ggcatcttgt tgtatataca tcatggttcc tctraaaaac 600
ttgtcttgcc akacgacctt acgt                                    624
```

<210> 31
<211> 145
<212> PRT
<213> Triticum sp.

<220>
<223> wheat DMT.4 615131 (861906 selclone ID)

<400> 31
Met Arg Ser Glu Cys Arg His Phe Ala Ser Ala Phe Ala Ser Ala Arg
 1   5   10   15

Leu Ala Leu Pro Ala Pro Gln Glu Lys Ser Leu Val Met Ser Ser Asn
            20   25   30

Gln Phe Ser Phe Gln Ser Gly Gly Met Pro Thr Pro Tyr Ser Thr Val
        35   40   45

Leu Pro Gln Leu Glu Gly Ser Ala Gln Gly Gln Asp Phe Cys Thr Asn
    50   55   60

Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro Ala Arg Glu Glu
65   70   75   80

Cys Pro Glu Thr Leu Glu Asn Asp Ile Glu Asp Tyr Asp Pro Asp Thr
                85   90   95

Gly Glu Ile Pro Leu Ile Lys Leu Asn Leu Gln Ala Phe Ala Gln Asn
            100   105   110

Leu Glu Asn Cys Ile Lys Glu Ser Asn Met Asp Leu Gly Ser Asp Asp
        115   120   125

Ile Ala Lys Ala Leu Val Ala Val Ser Thr Gly Ser Ala Ser Ile Pro
    130   135   140

Val
145

<210> 32
<211> 492
<212> DNA
<213> Triticum sp.

<220>
<223> wheat DMT.4 615131 (861906 selclone ID)

<400> 32
tacttttgga aaggtgttct gtacaaaaaa caagccaaat tgcaatgctt gtccaatgag 60
aagcgaatgc aggcatttcg caagtgcctt cgcaagtgca cggcttgcac ttcctgcacc 120
tcaggagaaa agtttggtga tgtcgagcaa tcaattcagt ttccagagtg gtggcatgcc 180
aactccatac tcaactgtgc ttcctcagct tgagggaagt gcccagggac aggatttttg 240
cactaacaat tcagagccaa ttattgagga gccagcaagt ccagcacggg aagaatgtcc 300
agaaactctt gaaaatgata ttgaagatta cgatccagat actggtgaaa tcccactaat 360
taagcttaac ttgcaagctt ttgctcagaa cttggaaaac tgcattaaag aaagcaatat 420
ggatcttggg tctgatgata tcgcgaaagc acttgttgct gttagcactg gatcagcttc 480
aattcctgtc cc   492

61

<210> 33
<211> 298
<212> PRT
<213> Glycine max

<220>
<223> soybean DMT.1 449122 (557119 selclone ID)

<220>
<221> MOD_RES
<222> (1)..(298)
<223> Xaa = any amino acid

<400> 33

```
Met Asp Ser Leu Asp Trp Asp Ala Val Arg Cys Ala Asp Val Ser Glu
 1               5                  10                  15

Ile Ala Glu Thr Ile Lys Glu Arg Gly Met Asn Asn Arg Leu Ala Asp
            20                  25                  30

Arg Ile Lys Asn Phe Leu Asn Arg Leu Val Glu Glu His Gly Ser Ile
        35                  40                  45

Asp Leu Glu Trp Leu Arg Asp Val Pro Pro Asp Lys Ala Lys Glu Tyr
    50                  55                  60

Leu Leu Ser Ile Arg Gly Leu Gly Leu Lys Ser Val Glu Cys Val Arg
65                  70                  75                  80

Leu Leu Thr Leu His His Leu Ala Phe Pro Val Asp Thr Asn Val Gly
                85                  90                  95

Arg Ile Ala Val Arg Leu Gly Trp Val Pro Leu Gln Pro Leu Pro Glu
            100                 105                 110

Ser Leu Gln Leu His Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Ile
        115                 120                 125

Gln Lys Tyr Leu Trp Pro Arg Leu Cys Lys Leu Asp Gln Glu Thr Leu
    130                 135                 140

Tyr Glu Leu His Tyr Gln Met Ile Thr Phe Gly Lys Xaa Phe Cys Thr
145                 150                 155                 160

Lys Ser Lys Pro Asn Cys Asn Ala Cys Pro Met Arg Xaa Glu Cys Arg
                165                 170                 175

His Phe Ala Ser Ala Phe Ala Ser Ala Arg Phe Ala Leu Pro Gly Pro
                180                 185                 190

Glu Gln Lys Ser Ile Val Ser Thr Thr Gly Asn Ser Val Ile Asn Gln
        195                 200                 205

Asn Pro Ser Glu Ile Ile Ser Gln Leu His Leu Pro Pro Pro Glu Asn
    210                 215                 220

Thr Ala Gln Glu Asp Glu Ile Gln Leu Thr Glu Val Ser Arg Gln Leu
225                 230                 235                 240

Glu Ser Lys Phe Glu Ile Asn Ile Cys Gln Pro Ile Ile Glu Glu Pro
                245                 250                 255
```

62

Arg Thr Pro Glu Pro Glu Cys Leu Gln Glu Ser Gln Thr Asp Ile Glu
260   265   270

Asp Ala Phe Tyr Glu Asp Ser Ser Glu Ile Pro Thr Ile Asn Leu Asn
275   280   285

Ile Glu Glu Phe Thr Leu Asn Leu Gln Asn
290   295

<210> 34
<211> 638
<212> DNA
<213> Glycine max

<220>
<223> soybean DMT.1 449122 (557119 selclone ID)

<400> 34
```
aataaaattt aakagcaagg aacaagaaaa agagaaaaag gatgaytttg actgggatag 60
tttaagaatt gaagcacagg ctaaggctgg gaaaagagaa aagacagata acaccatgga 120
ttctttggac tgggatgctg tgagatgtgc agatgtcagt gaaatcgctg agaccatcaa 180
agaaaggggc atgaacaaca ggcttgcaga tcgtattaag aatttcttaa atcgattggt 240
tgaagaacat ggaagcattg accttgaatg gcttagagac gttccacctg acaaagcaaa 300
agaatacttg ctcagcataa gaggattggg actaaaaagt gtggaatgtg tgcggctttt 360
aacactgcac catcttgcct tcccggtaga cacaaatgtc ggacgtatag cagtacgact 420
gggatgggtc cctctacagc cactgcctga gtcactgcag ttgcatctcc tagaattgta 480
cccagtgttg gagtcaatac aaaaatatct ctggcctcga ctatgcaagc tagatcagga 540
aacactatat gagctacatt accagatgat tacatttgga aaggkcttct gtacaaaaag 600
caaaccaaat tgtaatgcat gcccaatgag aggagaat                         638
```


<210> 35
<211> 251
<212> PRT
<213> Glycine max

<220>
<223> soybean DMT.2 387990 (473695 selclone ID)

<400> 35
Met Arg Met Thr Ile Asp Leu Val Ser Gln Gln Ser Leu Thr Ala Arg
1   5   10   15

Leu Gln Leu Ser Ile Leu Lys Asp Lys Leu Lys Ile Gln Cys Arg Lys
                20   25   30

Ala Arg Gly Leu Asp Phe Gly Arg Asn Glu Ser Ser Lys Ile Asp Ser
            35   40   45

Ser Pro Val Lys Leu Arg Ser Arg Glu His Gly Lys Glu Lys Lys Asn
        50   55   60

Asn Phe Asp Trp Asp Ser Leu Arg Ile Gln Ala Glu Ala Lys Ala Gly
65   70   75   80

Lys Arg Glu Lys Thr Glu Asn Thr Met Asp Ser Leu Asp Trp Asp Ala
                85   90   95

Val Arg Arg Ala Asp Val Ser Glu Ile Ala Asn Ala Ile Lys Glu Arg
            100   105   110

```
Gly Met Asn Asn Met Leu Ala Glu Arg Ile Gln Ser Phe Leu Asn Leu
    115                 120                 125

Leu Val Asp Lys His Gly Gly Ile Asp Leu Glu Trp Leu Arg Asp Val
    130                 135                 140

Pro Pro Asp Gln Ala Lys Glu Phe Leu Leu Ser Ile Arg Gly Leu Gly
145                 150                 155                 160

Leu Lys Ser Val Glu Cys Val Arg Leu Leu Thr Leu His His Leu Ala        ,
                165                 170                 175

Phe Pro Val Asp Thr Asn Val Gly Arg Ile Ala Val Arg Leu Gly Trp
                180                 185                 190

Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu His Leu Leu Glu
            195                 200                 205

Leu Tyr Pro Val Leu Glu Ser Ile Gln Lys Tyr Leu Trp Pro Arg Leu
    210                 215                 220

Cys Lys Leu Asp Gln Arg Thr Leu Tyr Glu Leu His Tyr Gln Leu Ile
225                 230                 235                 240

Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Lys
                245                 250


<210> 36
<211> 1134
<212> DNA
<213> Glycine max

<220>
<223> soybean DMT.2 387990 (473695 selclone ID)

<400> 36
gaaaagatag gatcattctc agatagcaac tcagaaatag aagacctgtc tagcgctgcc   60
aagtacaata gttattataa tagaatttct ttcagtgagc ttttagaaat ggcaagttca  120
accatgttgc atgaagttaa cagtcaaaga agcaaatcaa ctgagaactt aggagataca  180
tgtgatcagt ctatagacat gaagcatgac aacctggcag aaaacttgga aaaatcggat  240
gttactcaag gctccgcaga agcacccatc accaatggat atacttttaa aataacccca  300
aactcaggag tacttgaggt taactgttat gatcctctca aaatagaagt cccatcaagt  360
ggctcctcaa agggtaaaga tgagaatgac aatagatcta gtttcccaac agagtctgac  420
tgccaggctg caattgtcca ttctcaagga caaactgaag atccaatgca ggaaagcaag  480
gggactagat tttggtagga atgaaagcag taagatagat tcttcccctg taaaattaag  540
gagcagggag catggaaaag agaaaaagaa taactttgat tgggatagtt taagaataca  600
agcagaagct aaggcaggga aaagagaaaa gacagagaac accatggact ccttggactg  660
ggatgctgtt agacgcgcag atgtcagtga aattgccaat gcaatcaaag aaaggggcat  720
gaacaacatg cttgctgaac gtattcagag tttcctgaat ctattggttg acaagcatgg  780
gggcatcgat cttgagtggc tgagagatgt tccacctgat caagcaaaag aattcttgct  840
cagcataagg ggattgggat tgaaaagtgt ggagtgtgta cgactcttaa cactacacca  900
tcttgccttt ccggtggaca caaatgttgg acgtatagca gtaagattgg gatgggtgcc  960
tctccagcca ctgccagagt cactacagtt gcatcttcta gaattgtacc cagtgttgga 1020
gtccatacaa aaatatctct ggccccggct ctgcaagcta gaccaaagaa cattgtatga 1080
gctgcattac cagctgatta catttggaaa ggtcttctgt actaaaagca agcc        1134
```

64

<210> 37
<211> 209
<212> PRT
<213> Glycine max

<220>
<223> soybean DMT.3 657152 (546665 selclone ID)

<220>
<221> MOD_RES
<222> (1)..(209)
<223> Xaa = any amino acid

<400> 37

```
Ile Asn Gln Ala Glu Leu Gln Gln Thr Glu Val Ile Arg Gln Leu Glu
  1               5                  10                  15

Ala Lys Ser Glu Ile Asn Ile Ser Gln Pro Ile Ile Glu Glu Pro Ala
                 20                  25                  30

Thr Pro Glu Pro Glu Cys Ser Gln Val Ser Glu Asn Asp Ile Glu Asp
             35                  40                  45

Thr Phe Asn Glu Glu Ser Cys Glu Ile Pro Thr Ile Lys Leu Asp Ile
         50                  55                  60

Glu Glu Phe Thr Leu Asn Leu Gln Asn Tyr Met Gln Glu Asn Met Glu
 65                  70                  75                  80

Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu His Pro Gly
                 85                  90                  95

Ala Ala Cys Ile Pro Thr Pro Lys Leu Lys Asn Val Ser Arg Leu Arg
             100                 105                 110

Thr Glu His Tyr Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Asn
             115                 120                 125

Gly Trp Asn Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu Leu Ala
     130                 135                 140

Ile Trp Thr Pro Gly Glu Thr Ala Asx Ser Ile Gln Pro Pro Glu Ser
145                 150                 155                 160

Lys Cys Ser Ser Gln Glu Glu Cys Gly Xaa Leu Cys Asn Glu Asn Glu
                 165                 170                 175

Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Xaa Phe Xaa Asp Ser Xaa
             180                 185                 190

Arg Asp Thr Pro Asp Thr Met Ser Asn Ser Xaa Xaa Xaa Gly Ala Phe
         195                 200                 205

His
```

<210> 38
<211> 616
<212> DNA
<213> Glycine max

<220>
<223> soybean DMT.3 657152 (546665 selclone ID)

<400> 38
tataaaccaa gcagaacttc aacaaacaga agtgatcagg caactagaag caaaatctga 60
aatcaacatc agccaaccta ttattgaaga gccagcaact ccagagccag aatgctccca 120
agtatccgaa aatgatatag aggatacctt caatgaggaa tcatgtgaaa ttcccaccat 180
caaactagac atagaagagt tcactttgaa cttacaaaac tatatgcaag aaaacatgga 240
acttcaagaa ggtgaaatgt caaaggcctt ggttgctcta catccaggtg ctgcatgcat 300
tcctacaccc aagctgaaga atgtgagccg gttgcgaaca gagcattatg tttatgaact 360
ccctgattca catcccttc tgaatgggtg gaacaagcga gaacctgatg atccaggcaa 420
ataccttcta gctatatgga ctccagggga gacagcagat tctatacagc caccagaaag 480
caaatgcagc tctcaggaat gtggccggct ctgtaatgag aatgaatgtt tttcatgcaa 540
cagtttccgt gaagcaaggt tcacagatag ttcgagggac actcctgata ccatgtcgaa 600
cagctwtgar agggag 616

<210> 39
<211> 102
<212> PRT
<213> Glycine max

<220>
<223> soybean DMT.4 432980 (663678 selclone ID)

<400> 39
Glu Ala Ala Ser Ile Pro Met Pro Lys Leu Lys Asn Val Ser Arg Leu
 1   5   10   15

Arg Thr Glu His Cys Val Tyr Glu Leu Pro Asp Thr His Pro Leu Leu
                20   25   30

Gln Gly Trp Asp Thr Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu Leu
            35   40   45

Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro Glu
    50   55   60

Ser Lys Cys Ser Ser Gln Glu Glu Cys Gly Gln Leu Cys Asn Glu Asn
 65   70   75   80

Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
                85   90   95

Arg Gly Thr Leu Leu Val
            100

<210> 40
<211> 457
<212> DNA
<213> Glycine max

<220>
<223> soybean DMT.4 432980 (663678 selclone ID)

<400> 40
agaagctgct tccattccta tgcccaagct aaagaatgtg agccgattac gaacagagca 60
ttgtgtttat gaactcccag atacgcatcc tcttctccaa gggtgggaca cacgagagcc 120
tgatgatcca ggcaaatatc ttcttgctat atggactcca ggtgagacag caaattctat 180
acagccacca gaaagcaaat gcagctctca gaagaatgt ggccaactct gtaatgagaa 240

66

```
tgaatgtttc tcgtgcaaca gtttccgtga agcaaattct cagatagtta gagggacact 300
cctggtctga atgcttatca aaatcattgt tttaaccata tgtagcttac taattcttat 360
acattatggg aacaggggag ggaatacatc tccatagaaa ttcaagcatt ataatagact 420
gacttgaatt tatgataaat atgagcagat accatgt                          457
```

<210> 41
<211> 217
<212> PRT
<213> Medicago truncatula

<220>
<223> Medicago 6654943

<400> 41

```
Met Glu Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu Asn
  1               5                  10                  15

Gln Glu Ala Ser Tyr Ile Pro Thr Thr Lys Leu Lys Asn Val Ser Arg
              20                  25                  30

Leu Arg Thr Glu His Ser Val Tyr Glu Leu Pro Asp Ser His Pro Leu
          35                  40                  45

Leu Glu Gly Trp Glu Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu
      50                  55                  60

Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro
 65                  70                  75                  80

Asp Arg Arg Cys Ser Ala Gln Asp Cys Gly Gln Leu Cys Asn Glu Glu
                  85                  90                  95

Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
              100                 105                 110

Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser Phe
          115                 120                 125

Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His
      130                 135                 140

Glu Ser Ser Leu Asn Pro Ile Ser Val Pro Arg Ser Leu Ile Trp Asn
145                 150                 155                 160

Leu Asp Arg Arg Thr Val His Phe Gly Thr Ser Val Thr Ser Ile Phe
              165                 170                 175

Lys Gly Leu Ala Thr Pro Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe
              180                 185                 190

Val Cys Val Arg Ser Phe Glu Arg Ser Thr Arg Ala Pro Arg Pro Leu
          195                 200                 205

Met Ala Arg Leu His Phe Pro Ala Ser
    210                 215
```

<210> 42
<211> 657
<212> DNA
<213> Medicago truncatula

<220>
<223> Medicago 6654943 EST306265

<400> 42
gagaacatgg aacttcaaga aggtgaaatg tcaaaggcct tggttgctct aaatcaagaa 60
gcttcttaca ttcctacaac gaagctgaag aacgtgagtc ggttgcgcac agagcattct 120
gtttatgaac tcccagattc tcatcctctt ctggaagggt gggaaaagcg agaacctgat 180
gatccaggaa aataccttct agctatatgg acgccaggtg agactgcaaa ttctatacag 240
ccaccagaca gaagatgcag cgctcaagat tgtggccaac tctgtaatga ggaggaatgt 300
tttttcgtgca acagcttccg tgaagcaaat tcacagatag ttcgagggac aatcctgata 360
ccatgtcgaa cagctatgag agggagcttt ccgctaaacg gaacctattt tcaagtcaat 420
gaggtttttg cagaccatga atcaagtctt aatccgatta gcgttcccag aagtttgata 480
tggaaccttg ataggaggac agtgcatttt ggaacctccg taacaagcat attcaaaggt 540
ttagcaacac cagaaattca acagtgcttc tggagagggt ttgtctgtgt gcggagcttt 600
gaaaggtcaa cgagagcacc ccgtccttta atggccagac tgcatttccc agcaagc 657

<210> 43
<211> 210
<212> PRT
<213> Lycopersicon esculentum

<220>
<223> tomato 12624037

<400> 43
Met Glu Leu Gln Glu Gly Glu Met Ser Lys Ala Leu Val Ala Leu Asn
1   5   10   15

Gln Glu Ala Ser Tyr Ile Pro Thr Thr Lys Leu Lys Asn Val Ser Arg
                20   25   30

Leu Arg Thr Glu His Ser Val Tyr Glu Leu Pro Asp Ser His Pro Leu
            35   40   45

Leu Glu Gly Trp Glu Lys Arg Glu Pro Asp Asp Pro Gly Lys Tyr Leu
        50   55   60

Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser Ile Gln Pro Pro
65   70   75   80

Asp Arg Arg Cys Ser Ala Gln Asp Cys Gly Gln Leu Cys Asn Glu Glu
                85   90   95

Glu Cys Phe Ser Cys Asn Ser Phe Arg Glu Ala Asn Ser Gln Ile Val
            100   105   110

Arg Gly Thr Ile Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser Phe
        115   120   125

Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His
    130   135   140

Glu Ser Ser Leu Asn Pro Ile Ser Val Pro Arg Ser Leu Ile Trp Asn
145   150   155   160

68

```
Leu Asp Arg Arg Thr Val His Phe Gly Thr Ser Val Thr Ser Ile Phe
                  165             170             175

Lys Gly Leu Ala Thr Pro Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe
              180             185             190

Val Cys Val Arg Ser Phe Glu Arg Ser Thr Arg Ala Pro Arg Pro Leu
          195             200             205

Met Ala
    210
```

<210> 44
<211> 758
<212> DNA
<213> Lycopersicon esculentum

<220>
<223> tomato 12624037 EST469495

<400> 44
```
gcttgagaaa ggaagtccaa tcaaagagtg ggaaaaaaga aagaagcaag gatgcaatgg 60
actcattgaa ctacgaagca gtcagaagtg cagcagttaa agaaatttct gatgctatta 120
aggaacgagg gatgaacaac atgctggcag agcgaattaa ggacttcctc gatagactgg 180
tgagggatca tggaagtatt gacctagaat ggttgagaga tgtggcccca gacaaagcga 240
aagagtatct tttgagtatt cgtggactgg gtctgaaaag tgtagaatgt gtgcggctat 300
taacacttca taaccttgct tttccagttg acacaaatgt tggacgaata gctgtgagat 360
taggatgggt tcctctccaa ccacttcctg agtccctgca gttgcatctt cttgaactgt 420
atccaattct ggagtcaatt cagaagtatc tctggccacg actctgcaag ctcgatcaga 480
gaacactgta tgagttgcac taccacatga ttacctttgg aaaggttttc tgcaccaaaa 540
gtaagcctaa ctgtaatgca tgcccactga gagctgaatg cagacacttt gctagtgctt 600
acgcaagtgc aagacttgcc cttcctggcc cagaggagaa gagtatagtg agttcagcag 660
ttccgatccc tagtgaggga aatgcagctg ccgcattcaa gcccatgcta ttacccccag 720
agctgaagta gggatggcgt acccatatgc tccaattg                       758
```

<210> 45
<211> 203
<212> PRT
<213> Hordeum vulgare

<220>
<223> barley 13256964

<220>
<221> MOD_RES
<222> (1)..(203)
<223> Xaa = any amino acid

<400> 45
```
Met Ala Ser Glu Thr Glu Thr Phe Ala Phe Gln Ala Glu Ile Asn Gln
  1           5              10                  15

Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe
              20              25              30

Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Ile Arg
          35              40              45
```

```
Phe Glu Ser Leu Thr Asp Lys Ser Lys Leu Asp Ala Gln Pro Glu Leu
    50                  55              60
Phe Ile His Ile Ile Pro Asp Lys Ala Thr Asn Thr Leu Thr Leu Ile
65              70                  75                      80
Asp Ser Gly Ile Gly Met Thr Lys Ser Asp Leu Val Asn Asn Leu Gly
                85                  90                  95
Thr Ile Ala Arg Ser Gly Thr Lys Asp Phe Met Glu Ala Leu Ala Ala
            100             105             110
Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
        115             120             125
Ala Tyr Pro Cys Ala Glu Arg Val Xaa Val Thr Ser Lys His Asn Asp
    130             135             140
Asp Glu Gln Tyr Gly Gly Glu Xaa Gln Ala Gly Trp Leu Leu Tyr Cys
145             150             155             160
Gly His Val Ile Leu Leu Glu Ser Pro Phe Gly Gly Val Leu Arg Ser
            165             170             175
Pro Ser Thr Ser Arg Thr Asn Ser Trp Ser Thr Leu Glu Arg Arg Ala
            180             185             190
Phe Lys Asp Leu Gly Lys Asn Thr Pro Ser Ser
        195             200


<210> 46
<211> 883
<212> DNA
<213> Hordeum vulgare

<220>
<223> barley_13256964_HVSMEi0014B12f

<220>
<221> modified_base
<222> (1)..(883)
<223> n = g, a, c or t

<400> 46
cgagaacccc gctccaaagc cctaacccta ggccatcccc tctccctccc ctcaaccctc 60
gtcgactccg cgcgcgcctg cgttccagga gcttccgctg ccggcggcgc catggcctca 120
gagaccgaga ccttcgcctt ccaggcggag atcaaccagc tgctctcgct catcatcaac 180
accttctact ccaacaagga gatcttcctc cgcgagctca tctccaacgc ctccgatgcg 240
ttggataaga tcaggtttga gagcctcact gacaagagca agctggatgc tcagccagag 300
ctgttcatcc acattatccc tgacaaggcc accaacacac tcacccttat cgacagtggc 360
attggtatga ccaagtcaga cctcgtgaac aaccttggta ccattgcaag gtctggcacc 420
aaggatttca tggaggcatt ggctgctggt gccgatgtgt ccatgattgg tcagtttggt 480
gttggtttct actctgctta cccttgtgct gagagagtcg ntgtgaccag caagcacaac 540
gatgacgagc agtatggggg ggagtnccag gctgggtggc ttctttactg tggacacgtg 600
atactcttgg agagcccctt ggaggggta ctaagatccc cctctacctc aaggacgaac 660
agttggagta ccttggagag cgcgccttt aaggatttgg ggaaaaacac tccgagttca 720
taactttttc atctcctctg acggggaaa accctgaaa aggaatttt gcgctggaaa 780
gtgggtggaa aaatgggttc ctgggggggc ccggttgagg gattgttggt cacataaaca 840
actatcgtct tctatcttag cacctaatag tccttcacat gag 883
```

70

<210> 47
<211> 164
<212> PRT
<213> Zea mays

<220>
<223> corn BE511860

<400> 47
Leu Leu Glu Gly Phe Glu Gln Arg Glu Pro Asp Asp Pro Cys Pro Tyr
 1   5   10   15

Leu Leu Ser Ile Trp Thr Pro Gly Glu Thr Ala Gln Ser Ile Asp Ala
                20   25   30

Pro Lys Thr Phe Cys Asp Ser Gly Glu Thr Gly Arg Leu Cys Gly Ser
            35   40   45

Ser Thr Cys Phe Ser Cys Asn Asn Ile Arg Glu Met Gln Ala Gln Lys
        50   55   60

Val Arg Gly Thr Leu Leu Ile Pro Cys Arg Thr Ala Met Arg Gly Ser
65   70   75   80

Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp
                85   90   95

His Cys Ser Ser Gln Asn Pro Ile Asp Val Pro Arg Ser Trp Ile Trp
            100   105   110

Asp Leu Pro Arg Arg Thr Val Tyr Phe Gly Thr Ser Val Pro Thr Ile
            115   120   125

Phe Arg Gly Leu Thr Thr Glu Glu Ile Gln Arg Cys Phe Trp Arg Gly
            130   135   140

Phe Val Cys Val Arg Gly Phe Asp Arg Thr Val Arg Ala Pro Arg Ala
145   150   155   160

Leu Tyr Ala Arg

<210> 48
<211> 517
<212> DNA
<213> Zea mays

<220>
<223> corn BE511860 EST946063H01.Y1 946

<400> 48
tatgaactgc cagattcaca cgcctcttct ggaaggattc gaacagagag aaccagatga 60
tccctgtcca tatcttcttt ccatatggac cccaggtgaa actgcacaat cgatcgatgc 120
ccccaagaca ttctgtgatt caggggagac gggtagacta tgtggaagtt caacatgctt 180
tagttgcaac aatatacgag aaatgcaggc tcagaaagtc agaggaacac ttttgatacc 240
atgccgaaca gcaatgagag gaagcttccc acttaatggg acgtattttc aagttaatga 300
ggtatttgct gaccattgct caagtcaaaa tccaattgat gtcccacgaa gttggatttg 360
ggacctccca agacgaactg tttactttgg aacctcagtt cctacaatat tcagaggttt 420
aacgactgaa gagatacaac gatgcttttg gagaggattt gtttgcgtga ggggctttga 480
taggacagtg cgggcaccaa gggcccttta tgcaagg 517

71

<210> 49
<211> 137
<212> PRT
<213> Gossypium arboreum

<220>
<223> cotton 11206330

<400> 49
Met Gln Gly Asn Met Glu Leu Gln Glu Gly Asp Leu Ser Lys Ala Leu
1   5   10   15

Val Ala Leu Asn Pro Asp Ala Ala Ser Ile Pro Thr Pro Lys Leu Lys
                20   25   30

Asn Val Ser Arg Leu Arg Thr Glu His Tyr Val Tyr Glu Leu Pro Asp
            35   40   45

Lys His Pro Leu Leu Lys Gln Met Glu Lys Arg Glu Pro Asp Asp Pro
        50   55   60

Ser Pro Tyr Leu Leu Ala Ile Trp Thr Pro Gly Glu Thr Ala Asn Ser
65   70   75   80

Ile Gln Pro Pro Glu Gln Ser Cys Gly Ser Gln Glu Pro Gly Arg Leu
                85   90   95

Cys Asn Glu Lys Thr Cys Phe Ala Cys Asn Ser Val Arg Glu Ala Asn
            100   105   110

Thr Glu Thr Val Arg Gly Thr Ile Leu Ile Pro Cys Arg Asn Ala Met
            115   120   125

Arg Gly Ser Phe Ser Leu Asn Gly Thr
        130   135

<210> 50
<211> 766
<212> DNA
<213> Gossypium arboreum

<220>
<223> cotton 11206330 GA_Eb0023J04f

<400> 50
ctccgccagt gcataacttg cttaaagtag ggcctaatgt tggcaacaat gaacctatca 60
ttgaggagcc tgcaacacct gaaccagagc atgcagaagg atcagagagt gatattgaag 120
atgcaagcta tgatgatcca gatgaaattc ccacaataaa actcaacatt gaagagttca 180
cagcaaacct acagcattac atgcagggca atatggaact ccaagaaggg gacttgtcaa 240
aggctttagt agctttgaat cctgatgctg cttctatccc tactccaaaa ttgaagaatg 300
taagcaggct acgaacagag cactatgtat atgagcttcc agataaacat cctctcttga 360
aacagatgga aaagcgggaa cctgatgatc ctagccccta tcttcttgca atatggacac 420
caggtgaaac tgcaaactca attcaaccac cagaacaaag ttgtgggtcc caagaaccag 480
gaagactgtg caatgagaag acctgctttg cttgcaacag tgtaagagaa gctaacactg 540
agacagtccg aggaaccatc ttgatacctt gtagaaatgc aatgagagga agcttttccc 600
ttaatgggac ttaattttca agttaatgag gtcttttgca gatcatgaat caagcctcaa 660
cccaatcgac gttccaaggg gaatggattg ggaatttaac aagaacgaac tgtatacttg 720
gaacatcctg gttcatcaat atttaaagga cttttcgacg agggaa 766

72

<210> 51
<211> 179
<212> PRT
<213> Glycine max

<220>
<223> soybean 5606759

<220>
<221> MOD_RES
<222> (167)
<223> Xaa = His or Gln

<400> 51

```
Met Gly Trp Val Pro Leu Gln Pro Leu Pro Glu Ser Leu Gln Leu His
  1               5                  10                  15

Leu Leu Glu Leu Tyr Pro Val Leu Glu Ser Ile Gln Lys Tyr Leu Trp
             20                  25                  30

Pro Arg Leu Cys Lys Leu Asp Gln Glu Thr Leu Tyr Glu Leu His Tyr
         35                  40                  45

Gln Met Ile Thr Phe Gly Lys Val Phe Cys Thr Lys Ser Lys Pro Asn
     50                  55                  60

Cys Asn Ala Cys Pro Met Arg Ala Glu Cys Arg His Phe Ala Ser Ala
 65                  70                  75                  80

Phe Ala Ser Ala Arg Phe Ala Leu Pro Gly Pro Glu Gln Lys Ser Ile
                 85                  90                  95

Val Ser Thr Thr Gly Asn Ser Val Ile Asn Gln Asn Pro Ser Glu Ile
             100                 105                 110

Ile Ser Gln Leu His Leu Pro Pro Pro Glu Asn Thr Ala Gln Glu Asp
         115                 120                 125

Glu Ile Gln Leu Thr Glu Val Ser Arg Gln Leu Glu Ser Lys Phe Glu
     130                 135                 140

Ile Tyr Ile Cys Gln Pro Ile Ile Glu Glu Pro Arg Thr Pro Glu Pro
145                 150                 155                 160

Glu Cys Leu Gln Glu Ser Xaa Thr Asp Ile Glu Asp Ala Val Tyr Glu
                 165                 170                 175

Asp Ser Ser
```

<210> 52
<211> 583
<212> DNA
<213> Glycine max

<220>
<223> soybean 5606759 sb95c12.y1

<220>
<221> modified_base
<222> (546)
<223> n = g, a, c or t

<400> 52
acgagcttcc cggtagacac aaatgtcgga cgtattgccg tacgactggg atgggtgcct 60
ctgcagccac tgcctgagtc actgcagttg catctcctag aattgtaccc ggtgttggag 120
tcaatacaaa aatatctctg gcctcgactg tgcaagctag atcaggaaac actatatgag 180
ctacattacc agatggattac atttggaaag gtcttctgta caaaaagcaa accaaattgt 240
aatgcatgcc caatgagagc agaatgtaga cactttgcta gtgcatttgc aagtgcaagg 300
tttgcactgc ctggaccaga gcagaagagt atagttagca caactggaaa tagtgtgatt 360
aaccagaacc catctgaaat catcagtcag ttgcacttgc ctccacctga gaacacagcc 420
caagaagatg aaattcaact aacagaagtg agcagacaat tggaatcaaa atttgaaata 480
tatatttgcc aacctatcat tgaagagccc agaactccag agccagaatg cttgcaagaa 540
tcacanactg atatagagga tgctgtctat gaggattcaa gtg 583

<210> 53
<211> 155
<212> PRT
<213> Triticum aestivum

<220>
<223> wheat 12019155

<400> 53
Met Phe His Cys His Gly Thr Arg Gly Ser Asp Leu Gly Phe Asp Leu
1   5   10   15

Asn Lys Thr Pro Glu Gln Lys Ala Pro Gln Arg Arg Lys His Arg Pro
                20   25   30

Lys Val Ile Lys Glu Ala Lys Pro Lys Ser Thr Arg Lys Pro Ala Thr
            35   40   45

Gln Lys Thr Gln Met Lys Glu Asn Pro His Lys Lys Arg Lys Tyr Val
        50   55   60

Arg Lys Thr Ala Ala Thr Pro Gln Thr Asn Val Thr Glu Glu Ser Val
65   70   75   80

Asp Ser Ile Val Ala Thr Lys Lys Ser Cys Arg Arg Ala Leu Asn Phe
                85   90   95

Asp Leu Glu His Asn Lys Tyr Ala Ser Gln Ser Thr Ile Ser Cys Gln
            100   105   110

Gln Glu Ile Asp His Arg Asn Glu Lys Ala Phe Asn Thr Thr Ser Asp
            115   120   125

His Lys Ala Lys Glu Pro Lys Asn Thr Asp Asp Asn Thr Leu Leu Leu
            130   135   140

His Glu Lys Gln Ala Asn Asn Phe Gln Ser Glu
145   150   155

<210> 54
<211> 902
<212> DNA
<213> Triticum aestivum

<220>
<223> wheat 12019155 ESTBRY_901

<220>
<221> modified_base
<222> (1)..(902)
<223> n = g, a, c or t

<400> 54
```
aacagtcagg acaaaggcaa caagatcagc agtcaggaca agggcagcaa ccgggacaaa  60
ggcagccagg gtactactca acttctccgc aacaattagg acaaggccaa ccaaggtact 120
acccaacttc tccgcagcag ccaggacaag agcagcagcc aagacaattg caacaaccag 180
aacaagggca acaaggtcag cagccagaac aagggcagca aggtcagcag caaagacaag 240
gggagcaagg tcagcagcca ggacaagggc aacaagggca gcaaccggga caagggcagc 300
cagggtacta cccaacttct ccgcagcagt caggacaagg caaccaggg tactacccaa 360
cttctccaca gcagtcagga caattgcaac aaccagcaca agggcagcaa ccaggacaag 420
agcaacaagg tcaacagcca ggacaagggc agcaaccggg acaagggcaa gccagggtac 480
tacccaactt ctccgcagca gtcaggacaa gagcaacagc tagaacaatg gcaacagtca 540
ggacaggggc aaccagggca ctacccaact tctccgttgc aagccaggac aagggcaacc 600
agggtactac ccaacttctc acaacagata ggacaagggc agcagccaag aacaatttgc 660
acaaccaaca aagggcaac aagggcagc aaccaaggac aagggcaac aaggtcaaca 720
gcccangaaa aaaggcaaca aaggtcaagc aaccaagnac aagggggcagc aanccaggac 780
aagggcagcc anggtcctac ccaacttntt ttgagcaagt canggaaaag gggcaccanc 840
cnagganaaa tgggnaccac ccagnacaag gacaaccccg ggtcttcccc aaanttttn 900
cn                                                               902
```

<210> 55
<211> 255
<212> PRT
<213> Lycopersicon esculentum

<220>
<223> tomato 8106032

<220>
<221> MOD_RES
<222> (1)..(255)
<223> Xaa = any amino acid

<400> 55
```
Met Ser Leu Ala Ala His Phe Pro Leu Lys Thr Asp Ser Thr Gln Lys
 1               5                  10                  15

His Glu Gly Asn Thr Gly Ile Ile Ile Glu Glu Pro Glu Glu Cys Ala
            20                  25                  30

Thr Asp Pro Asn Val Ser Ile Arg Trp Tyr Glu Asp Gln Pro Asn Gln
        35                  40                  45

Ser Thr His Cys Gln Asp Ser Ser Gly Val Tyr Asn Thr Asp Ser Asn
    50                  55                  60

Glu Glu Lys Pro Ala Val Asn Asp Ser Glu Ser Ser Glu Asn Ser Thr
65                  70                  75                  80
```

Glu Cys Ile Lys Ser Ala Glu Cys Ser Val Ile Leu Gln Ser Asp Ser
                85   90   95

Ser Arg Glu Gly Ser Asp Leu Tyr His Gly Ser Thr Val Thr Ser Ser
                100   105   110

Gln Asp Arg Lys Glu Leu Asn Asp Leu Pro Ser Ser Pro Ser Ser Val
            115   120   125

Val Ser Ser Glu Ile Ser Ala Val Ile Gln Ala Ser Glu Gly Thr Asp
        130   135   140

Ser Ser Asn Phe Cys Ser Ser Thr Ser Phe Leu Lys Leu Leu Gln Met
145   150   155   160

Ala Gly Thr Ser Gly Ala Gln Gly Thr Arg Cys Thr Glu His Leu His
                165   170   175

Asn Gln His Lys Gly Asn Xaa Gly Gln Gln Pro Arg Thr Xaa Gly Asn
            180   185   190

Lys Val Asn Ser Pro Xaa Lys Lys Ala Thr Lys Val Lys Gln Pro Xaa
            195   200   205

Thr Arg Gly Ser Xaa Pro Gly Gln Gly Gln Pro Xaa Ser Tyr Pro Thr
    210   215   220

Xaa Phe Glu Gln Val Xaa Glu Lys Gly His Xaa Pro Arg Xaa Asn Gly
225   230   235   240

Xaa His Pro Xaa Gln Gly Gln Pro Arg Val Phe Pro Lys Xaa Phe
            245   250   255

<210> 56
<211> 589
<212> DNA
<213> Lycopersicon esculentum

<220>
<223> tomato 8106032 EST356474

<400> 56
ctcgtgccgg ttggggtata tcttacacag aatgtttcag atcacctttc tagttctgca 60
ttcatgtcac tcgctgccca ctttcctctg aaaacagaca gtactcagaa gcatgaagga 120
aatacaggta ttataattga agaacctgaa gagtgtgcaa cagaccccaa tgtttccatc 180
agatggtatg aagatcaacc aaatcagtca acccattgtc aggattcttc aggagtctat 240
aatacagatt caaatgaaga aaaaccagct gtcaatgact ctgaatcaag tgaaaatagc 300
acagaatgca taaaatcagc agaatgttct gtaattctgc aatcagattc ttctagagaa 360
ggctcagatc tgtatcatgg atcaacagtt acaagttccc aagatcgaaa agagttgaat 420
gatttgcctt cttctccgag ttctgttgtt cttctgaga tctctgctgt tattcaagct 480
tcagaaggaa ctgactcaag caacttttgc agctccactt cttttttgaa gctattacag 540
atggcaggaa cttcaggagc acaaggaacc aggtgcactg aacatctac 589

<210> 57
<211> 179
<212> PRT
<213> Zea mays

<220>
<223> corn AW042334

<400> 57
Asp Ala His Pro Leu Leu Gln Gln Leu Gly Leu Asp Gln Arg Glu His
1   5   10   15

Asp Asp Pro Thr Pro Tyr Leu Leu Ala Ile Trp Thr Pro Asp Gly Ile
            20   25   30

Lys Glu Ile Thr Lys Thr Pro Lys Pro Cys Cys Asp Pro Gln Met Gly
            35   40   45

Gly Asp Leu Cys Asn Asn Glu Met Cys His Asn Cys Thr Ala Glu Lys
        50   55   60

Glu Asn Gln Ser Arg Tyr Val Arg Gly Thr Ile Leu Val Pro Cys Arg
65   70   75   80

Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr Phe Gln Val
                85   90   95

Asn Glu Val Phe Ala Asp His Arg Ser Ser His Asn Pro Ile His Val
            100   105   110

Glu Arg Glu Met Leu Trp Asn Leu Gln Arg Arg Met Val Phe Phe Gly
        115   120   125

Thr Ser Val Pro Thr Ile Phe Lys Gly Leu Arg Thr Glu Glu Ile Gln
    130   135   140

Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Met Glu
145   150   155   160

Thr Arg Ala Pro Arg Pro Leu Cys Pro His Leu His Val Ile Ala Arg
                165   170   175

Pro Lys Ala

<210> 58
<211> 595
<212> DNA
<213> Zea mays

<220>
<223> corn AW042334 EST614027C01.y1 614

<400> 58
gaattcggca ccagcagatg cacatccact tttacaacag ctaggacttg accaacggga 60
acatgatgat cctaccccat acttattggc catatggaca ccagatggaa taaaggaaat 120
aactaagaca ccaaaaccat gctgtgaccc tcaaatggga ggcgatttat gcaataatga 180
aatgtgccac aattgtactg cagagaaaga aaaccaatct agatatgtca gaggcacaat 240
tctggttcct tgtcgaacag ctatgagggg tagtttccca cttaatggca cttactttca 300
agtcaatgag gtatttgctg accacagatc tagccacaac ccaatccatg tggaaaggga 360
gatgctatgg aacttgcaaa ggcgcatggt cttttcgggg acttcagtac ccaccatatt 420
caaaggtcta agaacagaag aaatacaaca atgcttctgg aggggatttg tctgtgtgcg 480
aggattcgac atggagacta gagcaccaag gcctctgtgc ccccatttgc acgttatagc 540
aaggccgaaa gcccgcaaga cagcagcaac tgagcaagta ctctaatcag caaag 595

77

<210> 59
<211> 150
<212> PRT
<213> Zea mays

<220>
<223> corn AW076298

<400> 59

```
Pro Cys Arg Thr Ala Met Arg Gly Ser Phe Pro Leu Asn Gly Thr Tyr
 1               5                  10                  15

Phe Gln Val Asn Glu Val Phe Ala Asp His Cys Ser Ser Gln Asn Pro
             20                  25                  30

Ile Asp Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val
         35                  40                  45

Tyr Phe Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Ser Thr Glu
     50                  55                  60

Gln Ile Gln Phe Cys Phe Trp Lys Gly Phe Val Cys Val Arg Gly Phe
 65                  70                  75                  80

Glu Gln Lys Thr Arg Ala Pro Arg Pro Leu Met Ala Arg Leu His Phe
                 85                  90                  95

Pro Ala Ser Lys Leu Lys Asn Asn Lys Leu Thr Thr Glu Glu Ile Gln
             100                 105                 110

Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg Thr
             115                 120                 125

Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro Ala Ser
     130                 135                 140

Lys Val Val Arg Gly Lys
145                 150
```

<210> 60
<211> 640
<212> DNA
<213> Zea mays

<220>
<223> corn AW076298 EST614065C03.y1 614

<400> 60

```
cggccccaga ccatgccgga cagcaatgag aggaagcttc ccacttaatg ggacatattt 60
tcaagttaat gaggtatttg ctgaccattg ttcaagccaa aatccaattg atgtcccacg 120
aagttggata tgggacctcc caagacgaac tgtttacttt ggaacctcag ttcctacaat 180
atttagaggt ttaacgactg aagagataca acaatgcttt tggagaggat tcgtttgtgt 240
gagggctttt gataggacag taagggcacc aaggcccctt tatgcaaggt tgcattttcc 300
tgccagcaag gttgttagag gcaaaaagcc tggagcggca agcgtcgaag aataataggt 360
acatcgaaga aatatagagg agctaacaaa acggatggat agccctaaat gagatgctga 420
cccaataagt cgccgaatca cctccaagtt ctaacccaat ttttgaggcg acatgacctg 480
ttaaattatg ttccatctat ggtaacagct tagatgttct tgtgagtcgc atattcttta 540
ctctgaaatt caatatagca aatgaaaaaa aacacagtgc atagtctagt tctaattgta 600
cctgtgagtg gaatcagttg ttgtacaaca tgaagatggg                      640
```

<210> 61
<211> 140
<212> PRT
<213> Zea mays

<220>
<223> corn BE639158

<400> 61
Lys Asn Ser Glu Pro Ile Ile Glu Glu Pro Ala Ser Pro Arg Glu Glu
  1   5   10   15

Arg Pro Pro Glu Thr Met Glu Asn Asp Ile Glu Asp Phe Tyr Glu Asp
              20   25   30

Gly Glu Ile Pro Thr Ile Lys Leu Asn Met Glu Ala Phe Ala Gln Asn
          35   40   45

Leu Glu Asn Cys Ile Lys Glu Ser Asn Asn Glu Leu Gln Ser Asp Asp
      50   55   60

Ile Ala Lys Ala Leu Val Ala Ile Ser Thr Glu Ala Ala Ser Ile Pro
 65   70   75   80

Val Pro Lys Leu Lys Asn Val Leu Arg Leu Arg Thr Glu His Tyr Val
                  85   90   95

Tyr Glu Leu Pro Asp Ala His Pro Leu Leu Gln Gln Leu Gly Leu Asp
             100   105   110

Gln Arg Glu His Asp Asp Pro Thr Pro Tyr Leu Leu Ala Ile Trp Thr
             115   120   125

Pro Asp Gly Ile Lys Glu Ile Thr Lys Thr Pro Lys
         130   135   140

<210> 62
<211> 561
<212> DNA
<213> Zea mays

<220>
<223> corn BE639158 EST946021E09.y1 946

<400> 62
tgagctgcat tatcagatga ttacatttgg aaaggtcttt tgtaccaaaa gacagccaaa 60
ttgcaatgca tgctatgaat tcgactcacc tacctcgcct tgaggggagt atccattcaa 120
gggagtttct tcctaagaat tcagagccaa taatcgagga gcctgcaagt ccaagagagg 180
aaagacctcc agaaaccatg gaaaatgata ttgaagattt ttatgaagat ggtgaaatcc 240
caacaataaa gcttaacatg gaagcttttg cacaaaactt ggagaattgc attaaagaaa 300
gcaataacga actccagtct gatgatattg caaaagcatt ggttgctatt agcactgaag 360
cagcttcgat tcctgtaccg aaactaaaga atgtgcttag cttcgaaca gaacactatg 420
tgtatgagct tccagatgca catccacttt tacaacagct aggacttgac caacgggaac 480
atgatgatcc taccccatac ttattggcca tatggacacc agatggaata aaggaaataa 540
ctaagacacc aaaaccatgc t 561

<210> 63
<211> 138
<212> PRT
<213> Zea mays

<220>
<223> corn T25243

<220>
<221> MOD_RES
<222> (63)
<223> Xaa = Asp or Glu

<220>
<221> MOD_RES
<222> (114)
<223> Xaa = Cys, Trp, Arg, Ser or Gly

<400> 63
```
Asn His Gln Pro Ile Ile Glu Glu Pro Leu Ser Pro Glu Cys Glu Thr
  1               5                  10                  15

Glu Asn Ile Glu Ala His Glu Gly Ala Ile Glu Asp Phe Phe Cys Glu
             20                  25                  30

Glu Ser Asp Glu Ile Pro Thr Ile Asn Leu Asn Ile Glu Glu Phe Thr
         35                  40                  45

Gln Asn Leu Lys Asp Tyr Met Gln Ala Asn Asn Val Glu Ile Xaa Tyr
     50                  55                  60

Ala Asp Met Ser Lys Ala Leu Val Ala Ile Thr Pro Asp Ala Ala Ser
 65                  70                  75                  80

Ile Pro Thr Pro Lys Leu Lys Asn Val Asn Arg Leu Arg Thr Glu His
                 85                  90                  95

Gln Val Tyr Glu Leu Pro Asp Ser His Pro Leu Leu Glu Gly Phe Glu
             100                 105                 110

Gln Xaa Glu Pro Asp Asp Pro Cys Pro Tyr Leu Leu Ser Ile Trp Thr
         115                 120                 125

Pro Gly Glu Leu His Asn Arg Ser Met Pro
     130                 135
```

<210> 64
<211> 422
<212> DNA
<213> Zea mays

<220>
<223> corn T25243 EST5c10h02

<220>
<221> modified_base
<222> (1)..(422)
<223> n = g, a, c or t

<400> 64
ctggtaatca tcagccaatc atcgaggaac cactgagccc agaatgtgaa actgaaaata 60
tagaggcaca tgagggtgca attgaggatt tcttttgtga agaatctgat gaaattccta 120
ccattaatct taatatcgag gagttcacac aaaacttgaa ggactatatg caagcaaaca 180
atgttgagat tgantatgct gacatgtcaa aggcattggt tgccatcacg cctgatgctg 240
cttccattcc aactccaaag ctcaagaatg tcaatcgtct gaggacagaa caccaagttt 300
atgaactgcc agattcacac cctcttctgg aaggattcga acagngngaa ccagatgatc 360
cctgtccata tcttctttcc atatggaccc caggtgaact gcacaatcga tcgatgcccc 420
aa   422

<210> 65
<211> 89
<212> PRT
<213> Zea mays

<220>
<223> corn AW453174

<400> 65
Phe Gln Gly Asn Glu Val Phe Ala Asp His Cys Ser Arg Gln Asn Pro
  1   5   10   15

Ile Asp Gly Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Gly
             20   25   30

Tyr Phe Gly Thr Ser Gly Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu
         35   40   45

Glu Ile Gln Arg Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe
     50   55   60

Asp Arg Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe
 65   70   75   80

Pro Val Ser Lys Val Val Arg Gly Lys
                 85

<210> 66
<211> 488
<212> DNA
<213> Zea mays

<220>
<223> corn AW453174 EST 660032D01.y1 660

<400> 66
catgccgaac agcaatgaga ggaagcttcc cacttaatgg gacgattttc aaggtaatga 60
ggtatttgct gaccattgct caaggcaaaa tccaattgat ggcccacgaa gttggatttg 120
ggaccttcca agacgaactg gttactttgg aacctcaggt cctacaatat tcagagggtt 180
aacgactgaa gagatacaac gatgcttttg gagaggattt gtttgcgtga ggggctttga 240
taggacagtg cgggcaccaa ggccccttta tgcaaggttg cattttcctg tcagcaaggt 300
tgttagaggc aaaaagcctg gagcagcaag agcagaagaa taatagaaca ttgaagaaat 360
ataggggtgc taaccagatg aggatggata gcccgaaatg agatgctgac ccaataggtc 420
gccaaatcac ctccaaattc taacccaatg acttccatct gtaatgaatg gcaatacctt 480
gaaaacct   488

<210> 67
<211> 93
<212> PRT
<213> Zea mays

<220>
<223> corn BE509759

<400> 67
Asn Gly Thr Tyr Phe Gln Val Asn Glu Val Phe Ala Asp His Arg Ser
 1   5   10   15

Ser His Asn Pro Ile His Val Glu Arg Glu Met Leu Trp Asn Leu Gln
                20   25   30

Arg Arg Met Val Phe Phe Gly Thr Ser Val Pro Thr Ile Phe Lys Gly
            35   40   45

Leu Arg Thr Glu Glu Ile Gln Gln Cys Phe Trp Arg Gly Phe Val Cys
        50   55   60

Val Arg Gly Phe Asp Met Glu Thr Arg Ala Pro Arg Pro Leu Cys Pro
 65   70   75   80

His Leu His Ile Ile Ala Arg Pro Lys Ala Arg Lys Thr
                85   90

<210> 68
<211> 570
<212> DNA
<213> Zea mays

<220>
<223> corn BE509759 EST946021E09.x1 946

<400> 68
tggcatctta catggactaa cagctagatg ctaatttaca tacagtagat ctgaaacaaa 60
aaagtgaaaa ttattggtgc ttcctgatgc ttcattagtc ctctcgtctc agaaactaac 120
agtctcggac cccatccatg gcttaaattt cctaaacaat ggctcttttt taggcaggaa 180
gtaatatgat tccatgcata ggtcgagagc tattgatgtc atatcacaat aaacatgatg 240
ttcataaaac tgatatcttt gctgattaga gtacttgctc agttgctgct gtcttgcggg 300
ccttcggcct tgctataatg tgcaaatggg ggcacagagg ccttggtgct ctagtctcca 360
tgtcgaatcc tcgcacacag acaaatcccc tccagaagca ttgttgtatt tcttctgttc 420
ttagaccttt gaatatggtg ggtactgaag tcccgaaaaa gaccatgcgc ctttgcaagt 480
tccatagcat ctcccttt cc acatggattg ggttgtggct agatctgtgg tcagcaaata 540
cctcattgac ttgaaagtaa gtgccattaa   570

<210> 69
<211> 71
<212> PRT
<213> Zea mays

<220>
<223> corn AW017984

<400> 69
Val Pro Arg Ser Trp Ile Trp Asp Leu Pro Arg Arg Thr Val Tyr Phe
 1   5   10   15

```
Gly Thr Ser Val Pro Thr Ile Phe Arg Gly Leu Thr Thr Glu Glu Ile
            20              25              30

Gln Gln Cys Phe Trp Arg Gly Phe Val Cys Val Arg Gly Phe Asp Arg
        35              40                  45

Thr Val Arg Ala Pro Arg Pro Leu Tyr Ala Arg Leu His Phe Pro Ala
    50              55              60

Ser Lys Val Val Arg Gly Lys
 65                 70
```

```
<210> 70
<211> 613
<212> DNA
<213> Zea mays

<220>
<223> corn AW017984 EST614065C03.x1 614

<400> 70
cctgaaacaa tcaaataacg gccgatgagg ttacattgtt tatagtatat gatcaaagaa 60
catgtatgac cattgtacaa ataggcccat cttcatgttg tacaacaact gattccactc 120
acaggtacaa ttagaactag actatgcact gtgttttttt tcatttgcta tattgaattt 180
cagagtaaag aatatgcgac tcacaagaac atctaagctg ttaccataga tggaacataa 240
tttaacaggt catgtcgcct caaaaattgg gttagaactt ggaggtgatt cggcgactta 300
ttgggtcagc atctcattta gggctatcca tccgttttgt tagctcctct atatttcttc 360
gatgtaccta ttattcttcg acgcttgccg ctccaggctt tttgcctcta acaaccttgc 420
tggcaggaaa atgcaacctt gcataaaggg gccttggtgc ccttactgtc ctatcaaagc 480
ccctcacaca aacgaatcct ctccaaaagc attgttgtat ctcttcagtc gttaaacctc 540
taaatattgt aggaactgag gttccaaagt aaacagttcg tcttgggagg tcccatatcc 600
aacttcgtgg gac                                                    613
```

```
<210> 71
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DMT Domain A
      consensus sequence

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ile or Leu

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Asp or Pro
```

```
<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Glu or Val

<220>
<221> MOD_RES
<222> (9)..(11)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Leu or Val

<220>
<221> MOD_RES
<222> (16)
<223> Xaa = Met or Leu

<220>
<221> MOD_RES
<222> (17)
<223> Xaa = Glu or Asp

<220>
<221> MOD_RES
<222> (18)..(19)
<223> Xaa = any amino acid, Xaa at positions 18 and 19
      may be present or absent

<220>
<221> MOD_RES
<222> (21)
<223> Xaa = Lys or Glu

<220>
<221> MOD_RES
<222> (22)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (23)
<223> Xaa = Lys or Thr

<220>
<221> MOD_RES
<222> (24)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (25)
<223> Xaa = Lys or Ala
```

```
<220>
<221> MOD_RES
<222> (26)
<223> Xaa = Trp or Lys


<220>
<221> MOD_RES
<222> (27)
<223> Xaa = Trp or Leu


<220>
<221> MOD_RES
<222> (28)
<223> Xaa = any amino acid


<220>
<221> MOD_RES
<222> (32)..(33)
<223> Xaa = any amino acid


<221> MOD_RES
<222> (35)
<223> Xaa = any amino acid


<221> MOD_RES
<222> (36)
<223> Xaa = Gly or Thr


<221> MOD_RES
<222> (38)
<223> Xaa = any amino acid


<221> MOD_RES
<222> (39)
<223> Xaa = Asp or Asn


<221> MOD_RES
<222> (40)
<223> Xaa = Ser or Leu


<221> MOD_RES
<222> (43)
<223> Xaa = Ala or Asn


<221> MOD_RES
<222> (46)
<223> Xaa = His or Arg


<221> MOD_RES
<222> (47)
<223> Xaa = any amino acid


<221> MOD_RES
<222> (48)
<223> Xaa = Val or Leu


<221> MOD_RES
<222> (51)
<223> Xaa = Asp or Asn
```

<221> MOD_RES
<222> (53)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (55)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (56)
<223> Xaa = Pro or Gln

<221> MOD_RES
<222> (66)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (74)
<223> Xaa = Val or Thr

<221> MOD_RES
<222> (76)
<223> Xaa = Val or Thr

<221> MOD_RES
<222> (77)
<223> Xaa = Leu or Ser

<221> MOD_RES
<222> (80)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (82)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (84)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (85)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (87)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (88)
<223> Xaa = any amino acid

<400> 71
Lys Val Xaa Xaa Asp Xaa Xaa Thr Xaa Xaa Xaa Trp Xaa Xaa Leu Xaa
  1   5   10   15

Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Arg Xaa
            20   25   30

Xaa Phe Xaa Xaa Arg Xaa Xaa Xaa Phe Ile Xaa Arg Met Xaa Xaa Xaa
        35   40   45

Gln Gly Xaa Arg Xaa Phe Xaa Xaa Trp Lys Gly Ser Val Val Asp Ser
    50   55   60

Val Xaa Gly Val Phe Leu Thr Gln Asn Xaa Asp Xaa Xaa Ser Ser Xaa
 65   70   75   80

Ala Xaa Met Xaa Xaa Ala Xaa Xaa Phe Pro
             85   90

<210> 72
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DMT Domain B
     consensus sequence

<221> MOD_RES
<222> (2)
<223> Xaa = Asp or Asn

<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (4)
<223> Xaa = Leu or Phe

<221> MOD_RES
<222> (6)..(10)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (12)..(17)
<223> Xaa = any amino acid, Xaa at positions 15-17 may be
     present or absent

<221> MOD_RES
<222> (19)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (20)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (21)
<223> Xaa = Asp or Asn

<221> MOD_RES
<222> (22)
<223> Xaa = Tyr or Trp

<221> MOD_RES
<222> (23)..(25)
<223> Xaa = any amino acid

```
<221> MOD_RES
<222> (27)..(36)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (38)..(39)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (42)
<223> Xaa = Met or Gln

<221> MOD_RES
<222> (43)
<223> Xaa = Asn or Phe

<221> MOD_RES
<222> (44)..(45)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (47)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (48)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (51)..(62)
<223> Xaa = any amino acid, Xaa at positions 53-62 may be
      present or absent

<221> MOD_RES
<222> (65)..(67)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (69)..(70)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (71)
<223> Xaa = His or Asn

<221> MOD_RES
<222> (73)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (81)..(82)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (83)
<223> Xaa = Pro or Asp

<221> MOD_RES
<222> (84)
<223> Xaa = Pro or Ser
```

```
<221> MOD_RES
<222> (85)
<223> Xaa = Asp or His

<221> MOD_RES
<222> (86)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (87)
<223> Xaa = Ala or Val

<221> MOD_RES
<222> (89)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (90)
<223> Xaa = Tyr or Phe

<221> MOD_RES
<222> (93)
<223> Xaa = Ser or Glu

<221> MOD_RES
<222> (94)
<223> Xaa = Ile or Phe

<221> MOD_RES
<222> (95)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (97)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (102)
<223> Xaa = Val or Ala

<221> MOD_RES
<222> (109)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (111)
<223> Xaa = His or Lys

<221> MOD_RES
<222> (112)..(113)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (125)
<223> Xaa = Ala or Cys

<221> MOD_RES
<222> (128)
<223> Xaa = Met or Leu
```

```
<221> MOD_RES
<222> (130)
<223> Xaa = Trp or Leu

<221> MOD_RES
<222> (134)
<223> Xaa = Gln or Glu

<221> MOD_RES
<222> (138)..(139)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (140)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (142)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (144)
<223> Xaa = Leu or Gln

<221> MOD_RES
<222> (146)
<223> Xaa = Glu or Phe

<221> MOD_RES
<222> (147)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (150)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (151)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (152)
<223> Xaa = Glu or Asp

<221> MOD_RES
<222> (153)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (154)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (166)
<223> Xaa = Asp or Pro

<221> MOD_RES
<222> (168)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (176)
<223> Xaa = Gln or His

<221> MOD_RES
<222> (177)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (183)..(184)
<223> Xaa = any amino acid, Xaa at positions 183 and 184
      may be present of absent

<221> MOD_RES
<222> (189)..(190)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (199)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (200)..(201)
<223> Xaa = any amino acid, Xaa at positions 200 and 201
      may be present or absent

<221> MOD_RES
<222> (204)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (205)
<223> Xaa = His or Tyr

<221> MOD_RES
<222> (206)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (207)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (210)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (211)
<223> Xaa = Ala or Val

<221> MOD_RES
<222> (212)..(221)
<223> Xaa = any amino acid, Xaa at positions 212-221 may
      be present or absent

<221> MOD_RES
<222> (223)
<223> Xaa = Ala or Ser
```

```
<221> MOD_RES
<222> (224)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (225)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (226)
<223> Xaa = Ala or Leu

<221> MOD_RES
<222> (228)
<223> Xaa = Pro or Glu

<221> MOD_RES
<222> (229)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (230)
<223> Xaa = Pro or Thr

<400> 72
Trp Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa
 1               5                   10                  15

Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa
        20                  25                  30

Xaa Xaa Xaa Xaa Ile Xaa Xaa Arg Gly Xaa Xaa Xaa Xaa Leu Xaa Xaa
        35                  40                  45

Arg Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu
    50                  55                  60

Xaa Xaa Xaa Val Xaa Xaa Xaa Gly Xaa Ile Asp Leu Glu Trp Leu Arg
65                  70                  75                  80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Leu Leu Xaa Xaa Xaa Gly
                85                  90                  95

Xaa Gly Leu Lys Ser Xaa Glu Cys Val Arg Leu Leu Xaa Leu Xaa Xaa
            100             105             110

Xaa Ala Phe Pro Val Asp Thr Asn Val Gly Arg Ile Xaa Val Arg Xaa
        115                 120             125

Gly Xaa Val Pro Leu Xaa Pro Leu Pro Xaa Xaa Xaa Gln Xaa His Xaa
    130             135             140

Leu Xaa Xaa Tyr Pro Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Leu Trp Pro
145             150             155                 160

Arg Leu Cys Lys Leu Xaa Gln Xaa Thr Leu Tyr Glu Leu His Tyr Xaa
            165             170                 175

Xaa Ile Thr Phe Gly Lys Xaa Xaa Phe Cys Thr Lys Xaa Xaa Pro Asn
            180             185                 190
```

92

Cys Asn Ala Cys Pro Met Xaa Xaa Xaa Glu Cys Xaa Xaa Xaa Xaa Ser
        195   200   205

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa
    210   215   220

Xaa Xaa Leu Xaa Xaa Xaa
225   230

<210> 73
<211> 292
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DMT Domain C
      consensus sequence

<221> MOD_RES
<222> (2)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (3)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (5)
<223> Xaa = Glu or Phe

<221> MOD_RES
<222> (7)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (8)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (10)..(14)
<223> Xaa = any amino acid, Xaa at positions 12-14 may
      be present or absent

<221> MOD_RES
<222> (16)..(30)
<223> Xaa = any amino acid, Xaa at positions 16-30 may
      be present or absent

<221> MOD_RES
<222> (31)
<223> Xaa = Asp or Ala

<221> MOD_RES
<222> (34)
<223> Xaa = Asp or Glu

<221> MOD_RES
<222> (35)..(57)
<223> Xaa = any amino acid, Xaa at positions 39-57 may
      be present or absent

```
<221> MOD_RES
<222> (58)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (60)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (62)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (63)
<223> Xaa = Leu or Phe

<221> MOD_RES
<222> (64)
<223> Xaa = Asn or Asp

<221> MOD_RES
<222> (65)..(81)
<223> Xaa = any amino acid, Xaa at positions 73-81 may
      be present or absent

<221> MOD_RES
<222> (82)
<223> Xaa = Ser or Ala

<221> MOD_RES
<222> (83)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (84)
<223> Xaa = Ala or Asp

<221> MOD_RES
<222> (87)..(94)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (95)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (97)..(101)
<223> Xaa = any amino acid, Xaa at positions 99-101 may
      be present or absent

<221> MOD_RES
<222> (102)
<223> Xaa = Lys or Arg

<221> MOD_RES
<222> (103)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (105)..(108)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (114)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (116)
<223> Xaa = Tyr or Phe

<221> MOD_RES
<222> (117)
<223> Xaa = Glu or Val

<221> MOD_RES
<222> (121)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (123)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (124)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (126)
<223> Xaa = Glu or Lys

<221> MOD_RES
<222> (127)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (128)
<223> Xaa = Asp or Glu

<221> MOD_RES
<222> (130)
<223> Xaa = Pro or Ile

<221> MOD_RES
<222> (131)..(132)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (136)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (139)
<223> Xaa = Thr or Gln

<221> MOD_RES
<222> (141)
<223> Xaa = Gly or Asp

<221> MOD_RES
<222> (142)
<223> Xaa = Glu or Gly
```

```
<221> MOD_RES
<222> (143)..(150)
<223> Xaa = any amino acid, Xaa at positions 149 and 150
      May be present or absent

<221> MOD_RES
<222> (151)
<223> Xaa = Pro or Ser

<221> MOD_RES
<222> (152)..(154)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (156)..(165)
<223> Xaa = any amino acid, Xaa at positions 162-165
      may be present or absent

<221> MOD_RES
<222> (166)
<223> Xaa = Met or Leu

<221> MOD_RES
<222> (168)..(171)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (173)..(174)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (176)..(178)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (179)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (181)..(185)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (186)
<223> Xaa = Val or Phe

<221> MOD_RES
<222> (190)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (192)..(213)
<223> Xaa = any amino acid, Xaa at positions 192-213
      may be present or absent

<221> MOD_RES
<222> (214)
<223> Xaa = Leu or Val
```

<221> MOD_RES
<222> (219)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (220)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (221)
<223> Xaa = Ser or Arg

<221> MOD_RES
<222> (222)..(223)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (226)..(228)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (229)
<223> Xaa = Arg or Thr

<221> MOD_RES
<222> (230)..(232)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (233)
<223> Xaa = Trp or Lys

<221> MOD_RES
<222> (234)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (236)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (237)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (239)..(242)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (244)
<223> Xaa = Thr or Ser

<221> MOD_RES
<222> (245)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (246)..(247)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (248)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (250)
<223> Xaa = Phe or Cys

<221> MOD_RES
<222> (251)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (252)
<223> Xaa = Gly or Leu

<221> MOD_RES
<222> (254)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (255)
<223> Xaa = Thr or Val

<221> MOD_RES
<222> (256)..(257)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (259)..(260)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (261)
<223> Xaa = Cys or Asn

<221> MOD_RES
<222> (263)
<223> Xaa = Trp or Gln

<221> MOD_RES
<222> (264)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (266)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (267)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (269)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (271)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (273)
<223> Xaa = Glu or Asp

<221> MOD_RES
<222> (274)..(276)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (277)
<223> Xaa = Arg or Gly

<221> MOD_RES
<222> (278)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (280)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (281)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (283)..(284)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (285)
<223> Xaa = Arg or His

<221> MOD_RES
<222> (288)..(289)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (290)
<223> Xaa = Ala or Val

<400> 73
Pro Xaa Xaa Glu Xaa Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Glu Xaa
 1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
            20   25   30

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Ile Xaa Xaa Xaa
    50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65   70   75   80

Xaa Xaa Xaa Xaa Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
                85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Leu Arg Thr Glu
            100   105   110

```
His Xaa Val Xaa Xaa Leu Pro Asp Xaa His Xaa Xaa Leu Xaa Xaa Xaa
        115             120             125

Asp Xaa Xaa Xaa Tyr Leu Leu Xaa Ile Trp Xaa Pro Xaa Xaa Xaa Xaa
        130             135             140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
145             150             155             160

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa
            165             170             175

Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Thr Xaa Leu Xaa
            180             185             190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            195             200             205

Xaa Xaa Xaa Xaa Xaa Xaa Phe Ala Asp His Xaa Xaa Xaa Xaa Xaa Pro
    210             215             220

Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Arg Xaa Xaa
225             230             235             240

Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Leu Xaa Xaa Xaa
            245             250             255

Xaa Ile Xaa Xaa Xaa Phe Xaa Xaa Gly Xaa Xaa Cys Xaa Arg Xaa Phe
        260             265             270

Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Leu Xaa Xaa Xaa Leu His Xaa
        275             280             285

Xaa Xaa Ser Lys
        290
```

<210> 74
<211> 1269
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DMT consensus
      sequence spanning Domains A, B and C

<221> MOD_RES
<222> (1)..(14)
<223> Xaa = any amino acid, Xaa at positions 10-14 may
      be present or absent

<221> MOD_RES
<222> (15)
<223> Xaa = Thr or Gln

<221> MOD_RES
<222> (16)
<223> Xaa = Ala or Ile

```
<221> MOD_RES
<222> (17)
<223> Xaa = Ser or Lys

<221> MOD_RES
<222> (18)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (19)..(21)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (22)
<223> Xaa = Ala or Arg

<221> MOD_RES
<222> (23)
<223> Xaa = Ser or Lys

<221> MOD_RES
<222> (24)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (25)
<223> Xaa = Gly or Met

<221> MOD_RES
<222> (26)..(27)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (28)
<223> Xaa = Ser or Arg

<221> MOD_RES
<222> (29)
<223> Xaa = Pro or Lys

<221> MOD_RES
<222> (30)..(31)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (32)
<223> Xaa = Lys or Phe

<221> MOD_RES
<222> (33)..(34)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (35)
<223> Xaa = Glu or Leu

<221> MOD_RES
<222> (37)
<223> Xaa = any amino acid, Xaa at position 37 may be
      present or absent
```

```
<221> MOD_RES
<222> (39)..(41)
<223> Xaa = any amino acid, Xaa at positions 39-41 may
      be present or absent

<221> MOD_RES
<222> (42)
<223> Xaa = Pro or Arg

<221> MOD_RES
<222> (43)..(44)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (45)
<223> Xaa = Pro or Arg

<221> MOD_RES
<222> (46)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (47)
<223> Xaa = Lys or Arg

<221> MOD_RES
<222> (48)
<223> Xaa = Lys or Arg

<221> MOD_RES
<222> (49)
<223> Xaa = Gly or Asp

<221> MOD_RES
<222> (50)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (51)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (52)
<223> Xaa = Gly or Val

<221> MOD_RES
<222> (53)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (54)
<223> Xaa = Lys or Gly

<221> MOD_RES
<222> (55)..(59)
<223> Xaa = any amino acid, Xaa at positions 58 and 59
      may be present or absent

<221> MOD_RES
<222> (60)
<223> Xaa = Pro or Ser
```

```
<221> MOD_RES
<222> (61)
<223> Xaa = Pro or Lys

<221> MOD_RES
<222> (62)..(64)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (65)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (66)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (67)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (68)..(69)
<223> Xaa = any amino acid, Xaa at positions 68 and 69
      may be present or absent

<221> MOD_RES
<222> (70)
<223> Xaa = Gln or Asp

<221> MOD_RES
<222> (71)..(79)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (80)
<223> Xaa = Pro or Gln

<221> MOD_RES
<222> (81)..(84)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (85)
<223> Xaa = Lys or Ala

<221> MOD_RES
<222> (86)
<223> Xaa = Pro or Ser

<221> MOD_RES
<222> (87)..(102)
<223> Xaa = any amino acid, Xaa at positions 100-102
      may be present or absent

<221> MOD_RES
<222> (103)
<223> Xaa = Pro or Ala

<221> MOD_RES
<222> (104)..(107)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (109)..(118)
<223> Xaa = any amino acid, Xaa at positions 109-118
      may be present or absent

<221> MOD_RES
<222> (120)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (121)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (122)..(125)
<223> Xaa = any amino acid, Xaa at positions 122-125
      may be present or absent

<221> MOD_RES
<222> (126)
<223> Xaa = Leu or Asn

<221> MOD_RES
<222> (127)..(172)
<223> Xaa = any amino acid, Xaa at positions 138-172
      may be present or absent

<221> MOD_RES
<222> (173)
<223> Xaa = Lys or Asp

<221> MOD_RES
<222> (174)..(180)
<223> Xaa = any amino acid, Xaa at positions 176-180
      may be present or absent

<221> MOD_RES
<222> (181)
<223> Xaa = Pro or Ala

<221> MOD_RES
<222> (184)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (185)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (187)
<223> Xaa = Asp or Pro

<221> MOD_RES
<222> (188)
<223> Xaa = Glu or Val

<221> MOD_RES
<222> (190)..(192)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (194)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (195)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (197)
<223> Xaa = Met or Leu

<221> MOD_RES
<222> (198)
<223> Xaa = Glu or Asp

<221> MOD_RES
<222> (199)..(200)
<223> Xaa = any amino acid, Xaa at positions 199 and 200
      may be present or absent

<221> MOD_RES
<222> (202)
<223> Xaa = Lys or Glu

<221> MOD_RES
<222> (203)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (204)
<223> Xaa = Lys or Thr

<221> MOD_RES
<222> (205)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (206)
<223> Xaa = Lys or Ala

<221> MOD_RES
<222> (207)
<223> Xaa = Trp or Lys

<221> MOD_RES
<222> (208)
<223> Xaa = Trp or Leu

<221> MOD_RES
<222> (209)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (210)
<223> Xaa = Glu or Lys

<221> MOD_RES
<222> (213)..(214)
<223> Xaa = any amino acid
```

<221> MOD_RES
<222> (216)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (217)
<223> Xaa = Gly or Thr

<221> MOD_RES
<222> (219)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (220)
<223> Xaa = Asp or Asn

<221> MOD_RES
<222> (221)
<223> Xaa = Ser or Leu

<221> MOD_RES
<222> (224)
<223> Xaa = Ala or Asn

<221> MOD_RES
<222> (227)
<223> Xaa = His or Arg

<221> MOD_RES
<222> (228)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (229)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (232)
<223> Xaa = Asp or Asn

<221> MOD_RES
<222> (234)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (236)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (237)
<223> Xaa = Pro or Gln

<221> MOD_RES
<222> (247)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (255)
<223> Xaa = Val or Thr

```
<221> MOD_RES
<222> (257)
<223> Xaa = His or Tyr

<221> MOD_RES
<222> (258)
<223> Xaa = Leu or Ser

<221> MOD_RES
<222> (261)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (263)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (265)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (266)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (268)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (269)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (272)..(287)
<223> Xaa = any amino acid, Xaa from positions 272-287
      may be present or absent

<221> MOD_RES
<222> (288)
<223> Xaa = Pro or Val

<221> MOD_RES
<222> (289)..(303)
<223> Xaa = any amino acid, Xaa at positions 295-303
      may be present or absent

<221> MOD_RES
<222> (304)
<223> Xaa = Ser or His

<221> MOD_RES
<222> (305)..(307)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (308)
<223> Xaa = Glu or Asp
```

```
<221> MOD_RES
<222> (309)..(332)
<223> Xaa = any amino acid, Xaa at positions 319-332
      may be present or absent

<221> MOD_RES
<222> (333)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (334)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (335)
<223> Xaa = Ser or Glu

<221> MOD_RES
<222> (336)..(341)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (342)
<223> Xaa = Lys or Asn

<221> MOD_RES
<222> (343)..(397)
<223> Xaa = any amino acid, Xaa at positions 351-397
      may be present or absent

<221> MOD_RES
<222> (398)
<223> Xaa = Glu or Ile

<221> MOD_RES
<222> (399)..(407)
<223> Xaa = any amino acid, Xaa at position 407 may be
      present or absent

<221> MOD_RES
<222> (408)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (409)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (410)
<223> Xaa = Asn or Ser

<221> MOD_RES
<222> (411)..(414)
<223> Xaa = any amino acid, Xaa at positions 412-414
      may be present or absent

<221> MOD_RES
<222> (415)
<223> Xaa = Glu or Asp
```

```
<221> MOD_RES
<222> (416)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (417)
<223> Xaa = Glu or Ser

<221> MOD_RES
<222> (418)..(421)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (422)
<223> Xaa = Gln or Leu

<221> MOD_RES
<222> (423)..(433)
<223> Xaa = any amino acid, Xaa at positions 423-433
      may be present or absent

<221> MOD_RES
<222> (434)
<223> Xaa = Asp or His

<221> MOD_RES
<222> (435)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (436)
<223> Xaa = Phe or Met

<221> MOD_RES
<222> (437)..(441)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (442)
<223> Xaa = Gln or Asn

<221> MOD_RES
<222> (443)..(445)
<223> Xaa = any amino acid, Xaa at positions 443-445
      may be present or absent

<221> MOD_RES
<222> (446)
<223> Xaa = Gly or Glu

<221> MOD_RES
<222> (447)..(448)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (449)
<223> Xaa = Gly or Asp

<221> MOD_RES
<222> (451)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (452)
<223> Xaa = Lys or Asp

<221> MOD_RES
<222> (453)..(463)
<223> Xaa = any amino acid, Xaa at positions 460-463
      may be present or absent

<221> MOD_RES
<222> (464)
<223> Xaa = Thr or Met

<221> MOD_RES
<222> (465)..(466)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (467)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (468)..(470)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (471)
<223> Xaa = Ser or Gln

<221> MOD_RES
<222> (472)..(481)
<223> Xaa = any amino acid, Xaa at positions 478-481
      may be present or absent

<221> MOD_RES
<222> (482)
<223> Xaa = Ser or Glu

<221> MOD_RES
<222> (483)..(485)
<223> Xaa = any amino acid, Xaa at position 485 may be present or absent

<221> MOD_RES
<222> (486)
<223> Xaa = Ser or Val

<221> MOD_RES
<222> (487)..(511)
<223> Xaa = any amino acid, Xaa at positions 506-511
      may be present or absent

<221> MOD_RES
<222> (512)
<223> Xaa = Thr or Ser

<221> MOD_RES
<222> (513)..(540)
<223> Xaa = any amino acid, Xaa at positions 529-540
      may be present or absent
```

```
<221> MOD_RES
<222> (541)
<223> Xaa = Arg or Ser

<221> MOD_RES
<222> (542)..(547)
<223> Xaa = any amino acid, Xaa at positions 544-547
      may be present or absent

<221> MOD_RES
<222> (548)
<223> Xaa = Thr or Pro

<221> MOD_RES
<222> (549)..(553)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (554)
<223> Xaa = Pro or Lys

<221> MOD_RES
<222> (555)..(564)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (565)
<223> Xaa = Gln or Glu

<221> MOD_RES
<222> (566)..(569)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (570)
<223> Xaa = Asp or Ser

<221> MOD_RES
<222> (571)..(574)
<223> Xaa = any amino acid, Xaa at positions 572-574
      may be present or absent

<221> MOD_RES
<222> (575)
<223> Xaa = Ser or Arg

<221> MOD_RES
<222> (576)..(580)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (581)
<223> Xaa = Asp or Pro

<221> MOD_RES
<222> (582)..(584)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (585)
<223> Xaa = Asn or Asp
```

<221> MOD_RES
<222> (586)..(588)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (589)
<223> Xaa = Pro or Tyr

<221> MOD_RES
<222> (590)..(591)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (592)
<223> Xaa = Phe or Ser

<221> MOD_RES
<222> (593)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (594)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (595)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (596)
<223> Xaa = Gly or Ser

<221> MOD_RES
<222> (597)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (598)
<223> Xaa = Ser or Ala

<221> MOD_RES
<222> (599)
<223> Xaa = Val or Arg

<221> MOD_RES
<222> (600)
<223> Xaa = Pro or Glu

<221> MOD_RES
<222> (601)..(603)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (604)
<223> Xaa = Thr or Ser

<221> MOD_RES
<222> (605)..(610)
<223> Xaa = any amino acid, Xaa at positions 608-610
      may be present or absent

```
<221> MOD_RES
<222> (611)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (612)..(614)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (615)
<223> Xaa = Pro or Glu

<221> MOD_RES
<222> (616)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (618)..(622)
<223> Xaa = any amino acid,Xaa at positions 621 and 622
      may be present or absent

<221> MOD_RES
<222> (623)
<223> Xaa = Leu or Gln

<221> MOD_RES
<222> (624)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (625)
<223> Xaa = Gly or Cys

<221> MOD_RES
<222> (626)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (627)
<223> Xaa = Ser or His

<221> MOD_RES
<222> (628)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (629)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (630)
<223> Xaa = Val or Gln

<221> MOD_RES
<222> (631)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (632)
<223> Xaa = Glu or Asp
```

```
<221> MOD_RES
<222> (633)..(635)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (637)
<223> Xaa = Gln or Glu

<221> MOD_RES
<222> (638)..(639)
<223> Xaa = any amino acid, Xaa at position 639 may be
      present or absent

<221> MOD_RES
<222> (640)
<223> Xaa = Asn or Gly

<221> MOD_RES
<222> (641)..(643)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (644)
<223> Xaa = Glu or Asn

<221> MOD_RES
<222> (645)..(674)
<223> Xaa = any amino acid, Xaa at positions 665-674
      may be present or absent

<221> MOD_RES
<222> (675)
<223> Xaa = Asn or Ala

<221> MOD_RES
<222> (676)
<223> Xaa = Pro or Gly

<221> MOD_RES
<222> (677)..(682)
<223> Xaa = any amino acid, Xaa at positions 678-682
      may be present or absent

<221> MOD_RES
<222> (683)
<223> Xaa = Ser or Leu

<221> MOD_RES
<222> (684)..(729)
<223> Xaa = any amino acid, Xaa at positions 709-729
      may be present or absent

<221> MOD_RES
<222> (730)
<223> Xaa = Gln or Asp

<221> MOD_RES
<222> (732)
<223> Xaa = Asp or Asn
```

<221> MOD_RES
<222> (733)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (734)
<223> Xaa = Leu or Phe

<221> MOD_RES
<222> (736)..(740)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (742)..(747)
<223> Xaa = any amino acid, Xaa at positions 745-747
      may be present or absent

<221> MOD_RES
<222> (749)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (750)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (751)
<223> Xaa = Asp or Asn

<221> MOD_RES
<222> (752)
<223> Xaa = Tyr or Trp

<221> MOD_RES
<222> (753)..(755)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (757)..(766)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (768)..(769)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (772)
<223> Xaa = Met or Gln

<221> MOD_RES
<222> (773)
<223> Xaa = Asn or Phe

<221> MOD_RES
<222> (774)..(775)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (777)
<223> Xaa = Ala or Ser

```
<221> MOD_RES
<222> (778)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (781)..(792)
<223> Xaa = any amino acid, Xaa at positions 783-792
      may be present or absent

<221> MOD_RES
<222> (795)..(797)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (799)..(800)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (801)
<223> Xaa = His or Asn

<221> MOD_RES
<222> (803)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (811)..(812)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (813)
<223> Xaa = Pro or Asp

<221> MOD_RES
<222> (814)
<223> Xaa = Pro or Ser

<221> MOD_RES
<222> (815)
<223> Xaa = Asp or His

<221> MOD_RES
<222> (816)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (817)
<223> Xaa = Ala or Val

<221> MOD_RES
<222> (819)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (820)
<223> Xaa = Tyr or Phe

<221> MOD_RES
<222> (823)
<223> Xaa = Ser or Glu
```

<221> MOD_RES
<222> (824)
<223> Xaa = Ile or Phe

<221> MOD_RES
<222> (825)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (827)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (832)
<223> Xaa = Val or Ala

<221> MOD_RES
<222> (839)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (841)
<223> Xaa = His or Lys

<221> MOD_RES
<222> (842)..(843)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (855)
<223> Xaa = Ala or Cys

<221> MOD_RES
<222> (858)
<223> Xaa = Met or Leu

<221> MOD_RES
<222> (860)
<223> Xaa = Trp or Leu

<221> MOD_RES
<222> (864)
<223> Xaa = Gln or Glu

<221> MOD_RES
<222> (868)..(869)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (870)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (872)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (874)
<223> Xaa = Leu or Gln

<221> MOD_RES
<222> (876)
<223> Xaa = Glu or Phe

<221> MOD_RES
<222> (877)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (880)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (881)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (882)
<223> Xaa = Glu or Asp

<221> MOD_RES
<222> (883)
<223> Xaa = Ser or Asn

<221> MOD_RES
<222> (884)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (887)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (896)
<223> Xaa = Asp or Pro

<221> MOD_RES
<222> (898)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (906)
<223> Xaa = Gln or His

<221> MOD_RES
<222> (907)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (913)..(914)
<223> Xaa = any amino acid, Xaa at positions 913 and 914
      may be present or absent

<221> MOD_RES
<222> (919)..(920)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (929)
<223> Xaa = Arg or Lys

```
<221> MOD_RES
<222> (930)..(931)
<223> Xaa = any amino acid, Xaa at positions 930 and 931
      may be present or absent

<221> MOD_RES
<222> (934)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (935)
<223> Xaa = His or Tyr

<221> MOD_RES
<222> (936)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (937)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (940)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (941)
<223> Xaa = Ala or Val

<221> MOD_RES
<222> (942)..(951)
<223> Xaa = any amino acid, Xaa at positions 942-951
      may be present or absent

<221> MOD_RES
<222> (953)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (954)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (955)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (956)
<223> Xaa = Ala or Leu

<221> MOD_RES
<222> (958)
<223> Xaa = Pro or Glu

<221> MOD_RES
<222> (959)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (960)
<223> Xaa = Pro or Thr
```

```
<221> MOD_RES
<222> (961)
<223> Xaa = Glu or Gln

<221> MOD_RES
<222> (962)..(977)
<223> Xaa = any amino acid, Xaa at positions 969-977
      may be present or absent

<221> MOD_RES
<222> (979)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (980)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (982)
<223> Xaa = Glu or Phe

<221> MOD_RES
<222> (984)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (985)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (987)..(991)
<223> Xaa = any amino acid, Xaa at positions 989-991
      may be present or absent

<221> MOD_RES
<222> (993)..(1007)
<223> Xaa = any amino acid, Xaa at positions 993-1007
      may be present or absent

<221> MOD_RES
<222> (1008)
<223> Xaa = Asp or Ala

<221> MOD_RES
<222> (1011)
<223> Xaa = Asp or Glu

<221> MOD_RES
<222> (1012)..(1034)
<223> Xaa = any amino acid, Xaa at positions 1016-1034
      may be present or absent

<221> MOD_RES
<222> (1035)
<223> Xaa = Ile or Val

<221> MOD_RES
<222> (1037)
<223> Xaa = any amino acid
```

```
<221> MOD_RES
<222> (1039)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1040)
<223> Xaa = Leu or Phe

<221> MOD_RES
<222> (1041)
<223> Xaa = Asn or Asp

<221> MOD_RES
<222> (1042)..(1058)
<223> Xaa = any amino acid, Xaa at positions 1050-1058
      may be present or absent

<221> MOD_RES
<222> (1059)
<223> Xaa = Ser or Ala

<221> MOD_RES
<222> (1060)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1061)
<223> Xaa = Ala or Asp

<221> MOD_RES
<222> (1064)..(1071)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1072)
<223> Xaa = Ile or Leu

<221> MOD_RES
<222> (1074)..(1078)
<223> Xaa = any amino acid, Xaa at positions 1076-1078
      may be present or absent

<221> MOD_RES
<222> (1079)
<223> Xaa = Lys or Arg

<221> MOD_RES
<222> (1080)
<223> Xaa = Leu or Met

<221> MOD_RES
<222> (1082)..(1085)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1091)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1093)
<223> Xaa = Tyr or Phe
```

<221> MOD_RES
<222> (1094)
<223> Xaa = Glu or Val

<221> MOD_RES
<222> (1098)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1100)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1101)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (1103)
<223> Xaa = Glu or Lys

<221> MOD_RES
<222> (1104)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1105)
<223> Xaa = Asp or Glu

<221> MOD_RES
<222> (1107)
<223> Xaa = Pro or Ile

<221> MOD_RES
<222> (1108)..(1109)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1113)
<223> Xaa = Ala or Ser

<221> MOD_RES
<222> (1116)
<223> Xaa = Thr or Gln

<221> MOD_RES
<222> (1118)
<223> Xaa = Gly or Asp

<221> MOD_RES
<222> (1119)
<223> Xaa = Glu or Gly

<221> MOD_RES
<222> (1120)..(1127)
<223> Xaa = any amino acid, Xaa at positions 1126 and 1127
     may be present or absent

<221> MOD_RES
<222> (1128)
<223> Xaa = Pro or Ser

```
<221> MOD_RES
<222> (1129)..(1131)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1133)..(1142)
<223> Xaa = any amino acid, Xaa at positions 1139-1142
      may be present or absent

<221> MOD_RES
<222> (1143)
<223> Xaa = Met or Leu

<221> MOD_RES
<222> (1145)..(1148)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1150)..(1151)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1153)..(1155)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1156)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (1158)..(1162)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1163)
<223> Xaa = Val or Phe

<221> MOD_RES
<222> (1167)
<223> Xaa = Leu or Ile

<221> MOD_RES
<222> (1169)..(1190)
<223> Xaa = any amino acid, Xaa at positions 1169-1190
      may be present or absent

<221> MOD_RES
<222> (1191)
<223> Xaa = Leu or Val

<221> MOD_RES
<222> (1196)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1197)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (1198)
<223> Xaa = Ser or Arg
```

```
<221> MOD_RES
<222> (1199)..(1200)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1203)..(1205)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1206)
<223> Xaa = Arg or Thr

<221> MOD_RES
<222> (1207)..(1209)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1210)
<223> Xaa = Trp or Lys

<221> MOD_RES
<222> (1211)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1213)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1214)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (1216)..(1219)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1221)
<223> Xaa = Thr or Ser

<221> MOD_RES
<222> (1222)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (1223)..(1224)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1225)
<223> Xaa = Ser or Thr

<221> MOD_RES
<222> (1227)
<223> Xaa = Phe or Cys

<221> MOD_RES
<222> (1228)
<223> Xaa = Arg or Lys
```

<221> MOD_RES
<222> (1229)
<223> Xaa = Gly or Leu

<221> MOD_RES
<222> (1231)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1232)
<223> Xaa = Thr or Val

<221> MOD_RES
<222> (1233)..(1234)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1236)..(1237)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1238)
<223> Xaa = Cys or Asn

<221> MOD_RES
<222> (1240)
<223> Xaa = Trp or Gln

<221> MOD_RES
<222> (1241)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1243)
<223> Xaa = Phe or Tyr

<221> MOD_RES
<222> (1244)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (1246)
<223> Xaa = Val or Leu

<221> MOD_RES
<222> (1248)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1250)
<223> Xaa = Glu or Asp

<221> MOD_RES
<222> (1251)..(1253)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1254)
<223> Xaa = Arg or Gly

<221> MOD_RES
<222> (1255)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1257)
<223> Xaa = Arg or Lys

<221> MOD_RES
<222> (1258)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1260)..(1261)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1262)
<223> Xaa = Arg or His

<221> MOD_RES
<222> (1265)..(1266)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (1267)
<223> Xaa = Ala or Val

<400> 74
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          20   25   30

Xaa Xaa Xaa Lys Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
               85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa
          100   105   110

Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          115   120   125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     130   135   140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145   150   155   160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
               165   170   175

```
Xaa Xaa Xaa Xaa Xaa Lys Val Xaa Xaa Asp Xaa Xaa Thr Xaa Xaa Xaa
            180             185             190

Trp Xaa Xaa Leu Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195             200             205

Xaa Xaa Glu Arg Xaa Xaa Phe Xaa Xaa Arg Xaa Xaa Xaa Phe Ile Xaa
    210             215             220

Arg Met Xaa Xaa Xaa Gln Gly Xaa Arg Xaa Phe Xaa Xaa Trp Lys Gly
225             230             235             240

Ser Val Val Asp Ser Val Xaa Gly Val Phe Leu Thr Gln Asn Xaa Asp
            245             250             255

Xaa Xaa Ser Ser Xaa Ala Xaa Met Xaa Xaa Ala Xaa Xaa Phe Pro Xaa
        260             265             270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        275             280             285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    290             295             300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305             310             315             320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        325             330             335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        340             345             350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        355             360             365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    370             375             380

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385             390             395             400

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        405             410             415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        420             425             430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        435             440             445

Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    450             455             460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465             470             475             480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            485             490             495
```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        500   505   510

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        515   520   525

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        530   535   540

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
545   550   555   560

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        565   570   575

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        580   585   590

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        595   600   605

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        610   615   620

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa
625   630   635   640

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        645   650   655

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        660   665   670

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        675   680   685

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        690   695   700

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
705   710   715   720

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Arg Xaa
        725   730   735

Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa
        740   745   750

Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa
        755   760   765

Xaa Arg Gly Xaa Xaa Xaa Xaa Leu Xaa Xaa Arg Ile Xaa Xaa Xaa Xaa
        770   775   780

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Val Xaa Xaa
785   790   795   800

Xaa Gly Xaa Ile Asp Leu Glu Trp Leu Arg Xaa Xaa Xaa Xaa Xaa Xaa
        805   810   815

```
Xaa Lys Xaa Xaa Leu Leu Xaa Xaa Xaa Gly Xaa Gly Leu Lys Ser Xaa
        820             825             830

Glu Cys Val Arg Leu Leu Xaa Leu Xaa Xaa Xaa Ala Phe Pro Val Asp
        835             840             845

Thr Asn Val Gly Arg Ile Xaa Val Arg Xaa Gly Xaa Val Pro Leu Xaa
    850             855             860

Pro Leu Pro Xaa Xaa Xaa Gln Xaa His Xaa Leu Xaa Xaa Tyr Pro Xaa
865             870             875             880

Xaa Xaa Xaa Xaa Gln Lys Xaa Leu Trp Pro Arg Leu Cys Lys Leu Xaa
            885             890             895

Gln Xaa Thr Leu Tyr Glu Leu His Tyr Xaa Xaa Ile Thr Phe Gly Lys
        900             905             910

Xaa Xaa Phe Cys Thr Lys Xaa Xaa Pro Asn Cys Asn Ala Cys Pro Met
        915             920             925

Xaa Xaa Xaa Glu Cys Xaa Xaa Xaa Xaa Ser Ala Xaa Xaa Xaa Xaa Xaa
    930             935             940

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa
945             950             955             960

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            965             970             975

Xaa Pro Xaa Xaa Glu Xaa Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Glu
        980             985             990

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    995             1000            1005

Ile Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    1010            1015            1020

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Ile Xaa Xaa
1025            1030            1035            1040

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        1045            1050            1055

Xaa Xaa Xaa Xaa Xaa Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        1060            1065            1070

Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Leu Arg Thr
        1075            1080            1085

Glu His Xaa Val Xaa Xaa Leu Pro Asp Xaa His Xaa Xaa Leu Xaa Xaa
    1090            1095            1100

Xaa Asp Xaa Xaa Xaa Tyr Leu Leu Xaa Ile Trp Xaa Pro Xaa Xaa Xaa
1105            1110            1115            1120

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
        1125            1130            1135
```

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
        1140                1145                1150

Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Thr Xaa Leu
      1155                1160                1165

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    1170                1175                1180

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Ala Asp His Xaa Xaa Xaa Xaa Xaa
1185                1190                1195                1200

Pro Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Arg Xaa
            1205                1210                1215

Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Leu Xaa Xaa
        1220                1225                1230

Xaa Xaa Ile Xaa Xaa Xaa Phe Xaa Xaa Gly Xaa Xaa Cys Xaa Arg Xaa
        1235                1240                1245

Phe Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Leu Xaa Xaa Xaa Leu His
    1250                1255                1260

Xaa Xaa Xaa Ser Lys
1265


<210> 75
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DMT conserved
      HhH-GPD motif

<400> 75
Asp Lys Ala Lys Asp Tyr Leu Leu Ser Ile Arg Gly Leu Gly Leu Lys
 1               5                10                15

Ser Val Glu Cys Val Arg Leu Leu Thr Leu His Asn Leu Ala Phe Pro
            20                25                30

Val Asp


<210> 76
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
      Xba-SKEN-7

<400> 76
cctctagagg aattgtcggc aaaatcgag                                    29
```

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-8

<400> 77
ggagagacgg ttattgtcaa cc   22

<210> 78
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-7

<400> 78
aaaagtctac aagggagaga gagt   24

<210> 79
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-5

<400> 79
gtagatgtac atacgtacc   19

<210> 80
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-8

<400> 80
gcatcctcca acaagtaaca atccactc   28

<210> 81
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-6

<400> 81
cactgagatt aattcttcag actcg   25

131

<210> 82
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-3.5

<400> 82
ctcaggcgag tcaatgccgg agaacac   27

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-3

<400> 83
cgagggctga tccggggggat agatatttt   29

<210> 84
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-2

<400> 84
cccccggatc agccctcgaa ttc   23

<210> 85
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-1

<400> 85
cccctgtcta caaattcacc acctgg   26

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEL-4

<400> 86
ctgacccaac tgcttctctt c   21

<210> 87
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer skes1.5

<400> 87
tcacctgttc tgaacagact gg   22

<210> 88
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-1.4

<400> 88
cagcagacga gtccataatg ctctgc   26

<210> 89
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-2.4

<400> 89
ggtttgcctt ccacgaccac c   21

<210> 90
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-1

<400> 90
ggaagccacg caaagctgca actcagg   27

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
     SKES-2.45

<400> 91
gagttgcagc tttgcgtggc ttcc   24

```
<210> 92
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES2.5

<400> 92
ttcagactca gagtcacctt gc                                          22


<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-2

<400> 93
accagcagcc ttgcttggcc                                             20


<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-3

<400> 94
catgccagag aagcagggct cc                                          22


<210> 95
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES3.5

<400> 95
cgatgatact gtctcttcga gc                                          22


<210> 96
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-6

<400> 96
cctccgcctg ctcatgcctc ag                                          22
```

<210> 97
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-4

<400> 97
gtccatcagg agaacttctg tgtcaggat   29

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-4

<400> 98
gggaacaagt gcaccatctc c   21

<210> 99
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-6

<400> 99
gctctcatag ggaacaagtg caccatctc   29

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKES-5

<400> 100
cgctcgcatg cacctggtac   20

<210> 101
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-1

<400> 101
ggagggaatc gagcagctag ag   22

<210> 102
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-2

<400> 102
gagcagctaa gggactgttc aaactc   26

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-3

<400> 103
ccaggaatgg gattgtccgg   20

<210> 104
<211> 22
<212> DNA ·
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer 3'RACE-2

<400> 104
cttggacggc gcttgaggaa cc   22

<210> 105
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer 3'RACE-1

<400> 105
gcctacaagc cagtgggata g   21

<210> 106
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-1

<400> 106
gccaaggact atctcttgag c   21

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKB-4

<400> 107
ggatggactc gagcactggg   20

<210> 108
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKE2.2-4

<400> 108
agaggagagt gcagacactt tg   22

<210> 109
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-3

<400> 109
gaggaccctg acgagatccc aac   23

<210> 110
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-9

<400> 110
ccatgtgttc ccgtagagtc attcc   25

<210> 111
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
      2.2+SKE-1

<400> 111
atggagctcc aagaaggtga catg   24

<210> 112
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-5

<400> 112
cagaagtgtg gagggaaagc gtctggc   27

<210> 113
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-4

<400> 113
ccctcagact gttacactca gaac   24

<210> 114
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-2

<400> 114
cccgttgagc ggaaaacttc ctctcatggc   30

<210> 115
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-7

<400> 115
ggaaaggatt cgtatgtgtc cgtgg   25

<210> 116
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SKEN-5

<400> 116
gcaatgcgtt tgctttcttc cagtcatct   29

```
<210> 117
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-6

<400> 117
gaggagagca gagaagcaat gcgtttgc                                    28


<210> 118
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer cDNA-8

<400> 118
gttagagaga aaataaataa ccc                                         23


<210> 119
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
      2.2+SKE-3

<400> 119
ccgtaaacaa caccggatac ac                                          22
```